

(a) (b) (c) (d) (e) (f)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:03:26 1996; MasPar time 11.71 Seconds

607.114 Million cell updates/sec

Tabular output not generated

Title: >US-08-446-915-2
Description: (1-409) from US08446915.pep

Sequence: 1 MASSAPDENEFQEGCPAP.....KHAYVKDDTMFKCIVDTSA 409

Scoring table: PAM 150

Searched: 49340 seqs, 17385503 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Database: swiss-prot32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9
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Statistics: Mean 49.616; Variance 101.312; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2945	100.0	409	8	TRF1_MOUSE	THE RECEPTOR ASSOCIAT	0.00e+00
2	972	33.0	501	8	TRF2_MOUSE	THE RECEPTOR ASSOCIAT	3.50e-16
3	148	5.0	760	5	MEP1_MOUSE	MEP1RAN A ALPHA-SUBUNIT	7.90e-07
4	127	4.3	1048	7	SBCC_ECOLI	EXONUCLEASE SBCC.	7.06e-04
5	120	4.1	1291	7	SPCB_DROME	SPECTRIN BETA CHAIN.	6.00e-03
6	115	3.9	1319	3	DY15_DROME	150 KD DYNEIN--ASSOCIA	2.65e-02
7	112	3.8	493	4	INVO_SARGO	INVOLINCRIN.	6.33e-02
8	112	3.8	870	6	POL_TSRV	POL. POLYPROTEIN (REVE	6.33e-02
9	113	3.8	1427	7	REST_HUMAN	RESTIN (CYTOPLASMIC L	4.78e-02
10	109	3.7	544	4	INVO_ADONI	INVOLINCRIN.	1.49e-01
11	106	3.6	668	5	MEP1_RAT	MEP1RAN A BETA-SUBUNIT	3.44e-01
12	105	3.6	716	1	ARCB_ECOLI	AEROBIC RESPIRATION C	4.55e-01
13	107	3.6	2663	2	CENB_HUMAN	CENTROMERIC PROTEIN E	2.61e-01

14	102	3.5	428	4	INVO_CEBL	INVOLODRIN.	1.02e+00
15	103	3.5	443	6	PC1_HUMAN	PARAMOPLASTIC CEREBE	7.82e-01
16	103	3.5	467	3	FUMC_ECOLI	FORMATE HYDRATASE CL	7.82e-01
17	104	3.5	741	1	BSCG_DROME	BLASTOGEN SPECIFIC P	5.96e-01
18	103	3.5	872	8	ULF4_HSV24	97 KD ALPHA TRANS-IND	7.82e-01
19	103	3.5	2017	5	MYSN_DROME	MYOSIN HEAVY CHAIN, N	7.82e-01
20	100	3.4	92	9	Y108_SSV1	HYPOTHETICAL 10.8 KD	1.75e+00
21	99	3.4	312	9	VPHE_HSPV1	POLYHEDRAL ENVELOPE P	2.27e+00
22	99	3.4	333	8	VG24_NSVD	HYPOTHETICAL GENE 24	2.27e+00
23	101	3.4	522	4	INVO_HYLLA	INVOLODRIN.	1.34e+00
24	100	3.4	560	4	INVO_PANDA	INVOLODRIN.	1.75e+00
25	101	3.4	567	7	RECK_ECOLI	DNA REPAIR PROTEIN RE	1.34e+00
26	100	3.4	567	5	NARH_HAEIN	SENSOR PROTEIN NARQ H	1.75e+00
27	101	3.4	917	7	SLAP_THETH	S-LAYER PROTEIN PRECU	1.34e+00
28	99	3.4	1053	3	DYNA_CHICK	DYNACTIN, 117 KD ISOE	2.27e+00
29	101	3.4	1335	3	DYNA_RAT	DYNACTIN, 150 KD ISOE	1.34e+00
30	101	3.4	1505	2	CDP_HUMAN	CCAAT DISPLACEMENT PR	1.34e+00
31	99	3.4	2833	4	IP3B_DROME	INOSITOL 1,4,5-TRISP	2.27e+00
32	98	3.3	236	8	VC05_SPVNA	HYPOTHETICAL PROTEIN	2.95e+00
33	98	3.3	312	1	CA4H_HUMAN	CARBONIC ANHYDRASE IV	2.95e+00
34	98	3.3	363	1	BASS_ECOLI	SENSOR PROTEIN BASS/P	2.95e+00
35	98	3.3	450	4	IFEEF_HELPO	NON-NEURONAL CYTOL	2.95e+00
36	98	3.3	458	8	VIM1_XENLA	VIMENTIN 1 AND 2.	2.95e+00
37	98	3.3	564	5	M12_STRPY	M PROTEIN, SEROTYPE 1	2.95e+00
38	96	3.3	575	4	IFER_HELAS	MITOCHONDRIAL CYTOL	4.95e+00
39	97	3.3	577	5	MEPI_NEDCR	MITOCHONDRIAL PROCESS	4.95e+00
40	98	3.3	876	5	MYSS_HUMAN	MYOSIN HEAVY CHAIN, S	2.95e+00
41	98	3.3	962	2	COPB_DROME	COTOPHER BETA SUBUNIT	2.95e+00
42	97	3.3	974	5	MYSD_MESAU	MYOSIN HEAVY CHAIN, C	3.83e+00
43	97	3.3	1569	6	PHP_DROME	POLYHEDROECT-PROXIMAL	3.83e+00
44	97	3.3	1938	5	MYSS_AQDIR	MYOSIN HEAVY CHAIN, S	3.83e+00
45	96	3.3	1939	5	MYSN_CHICK	MYOSIN HEAVY CHAIN, N	4.95e+00

ALIGNMENTS

RESULT	1	STANDARD;	PR;	409 AA.
ID	TRF1 MOUSE			
AC	P39428;			
DT	01-FEB-1995 (REL. 31, CREATED)			
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)			
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)			
DE	TNF RECEPTOR ASSOCIATED FACTOR 1 (TRAF1).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
NC	(1)			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND 390-402.			
RX	MEDLINE; 9434937L.			
RA	ROTHE M., WONG S.C., HENZEL W.J., GOEDEL D.V.;			
RL	CELL. 78:681-692(1994).			
CC	-1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN			
CC	OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.			
DR	EMBL; L35302; L35302.			
FM	COILED COIL.			
SQ	SEQUENCE 409 AA; 4546 MW; 857196 CN;			
Query Match	100.0%;	Score 2945;	DB 8;	Length 409;
Best Local Similarity	100.0%;	Pred. No. 0.00e+00;		
Matches 409;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Y 1 MASSAPENEFQCCPAPCCDSEPRVLCCTACISENLBDDRLICPKGADNLPYS 60
D 61 pgsplqeqvhsdvaeeaimpcfiagvcsfkyqpsqmqeateqsehllylllavlkewk 120
Y 61 pgsplqeqvhsdvaeeaimpcfiagvcsfkyqpsqmqeateqsehllylllavlkewk 120
D 121 sspgsnlqgaamalernleelqlqaaveatqglevdcyrapccesqeelaqlhlyvekll 180
Y 121 SSGPSNLQGAAMALERNLEELQLQAAVEATQGLEVDCTRAPCCESQEELAQLHLYVEKLL 180
D 181 aqleeklrifanivavlnkveeahlalaasihgsqldrehllalegrvvelqgtlaqkd 240
Y 181 AQLEEKLRIFANIVAVLNKVEEAHLALAAASHHQSQLDREHLLLEGRVVELQGTLAQKQD 240
D 241 qvlgqlkhehlrlmeaeafdgftlkintkrcheevgrvtalsfpafytakygkklcl 300
Y 241 QVLGQLKHEHLRLMEAEAFDGTFLMKITNTVKRCHESVCGRTVLSFPAFYTAKYGYKLCL 300
D 301 rlylmgdsggkthllslfivlmrgcydalpwpfrnkvtfmlldqnrehajdafprdlis 360
Y 301 RLYLMGDSGKTHLSLFIVLMRGEDALPWPFRNKVTFMLLDQNNREHAIDAFPRDLIS 360
D 361 saefqrpgqetnvaagcplffipleklsqpkhavykddtmfklciydvsa 409
Y 361 SAEFQRPGQETNVAAGCPLFFIPLEKLSQPKHAYVKDDTMFLKCIYDVSAA 409
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RESULT 2

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ID TRE2 MOUSE STANDARD; PRT; 501 AA.
AC P39429;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DE TNF RECEPTOR ASSOCIATED FACTOR 2 (TNFAF2).
OS MUS MUSCULUS (MOUSE).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94349371.
RA ROTHE M., MONG S.C., HENZEL W.J., COEDDEL D.V.;
RL CELL 78:681-692(1994).
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; L35303; L35303.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4.
KM ZINC-FINGER; COILED COIL.
FT ZN FING 34 72 C3HC4-TYPE.
SQ SEQUENCE 501 AA; 56026 MW; 1264825 CN;
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Query Match 33.0%; Score 972; DB 8; length 501;
Best Local Similarity 54.0%; Pred. No. 3,50e-163;
Matches 121; Conservative 61; Mismatches 41; Indels 1; Gaps 1;

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D 275 leqistatfenivcylnevevavtaeasqrhldqkiealeankqqlersiglkdia 334
Y 183 LEEKLVEFANIVAVLNKVEASHLALASIHQSQLDREHLLLEGRVVELQGTLAQKQD 242
D 335 madleqvaevaydydvfwiklsdftkrqevagrtpalfpafyerygykmlctiv 394
Y 335 MADLEQVAEVAYDYDVFWIKLSDFTKRQEVAGRTPALFPAFYERYGYKMLCTIV 394
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Y 243 LGLKLESHRLMEASFDGTFLMKITNTVKRCHESVCGRTVLSFPAFYTAKYGYKLRL 302
D 395 ylngdgrgthslslfivmkgpndallpwpfrnkvtfmlldqnrehajdafprdas 454
Y 303 YLMGDSGKTHLSLFIVLMRGEDALPWPFRNKVTFMLLDQNNREHAIDAFPRDLISA 362
D 455 sfqrpsdmlnaagcplfcvyskmae-knsyvrddalifikaivd 497
Y 363 SFQRPSDMLNAGCPLFCVYSKMAE-KNSYVRDDALIFIKAIYD 406
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RESULT 3

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ID MEPA MOUSE STANDARD; PRT; 760 AA.
AC P28825;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-NOV-1992 (REL. 32, LAST ANNOTATION UPDATE)
DE MEPRIN A ALPHA-SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEPTIDASE-2)
DE (MEP-1).
GN MEPA.
OS MUS MUSCULUS (MOUSE).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=C57BL/6, AND C3H/HE; TISSUE=KIDNEY;
RX MEDLINE; 92250517.
RA JIANG W., GORBEA C.M., FLANNERY A.V., BEYON R.J., GRANT G.A.,
RA BOND J.S.;
RL J. BIOL. CHEM. 267:9185-9193(1992).
RN [2]
RP SEQUENCE OF 77-275 FROM N.A.
RX MEDLINE; 92042028.
RA DUMEROUTH E., STERCH E.E., JIANG W., WOLZ R.L., BOND J.S.,
RA FLANNERY A.V., BEYON R.J.;
RL J. BIOL. CHEM. 266:21381-21385(1991).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE; 91355206.
RA WOLZ R.L., HARRIS R.B., BOND J.S.;
RL BIOCHEMISTRY 30:8488-8493(1991).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEIN AND PEPTIDE SUBSTRATES
CC PREFERENTIALLY ON CARBOXYL SIDE OF HYDROPHOBIC RESIDUES.
CC -1- COFACTOR: ZINC.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SUBUNIT: HOMOTETRAMER OF ALPHA OR BETA SUBUNITS; HETEROTETRAMER
CC OF TWO ALPHA AND TWO BETA SUBUNITS ARE FORMED BY NON-COVALENT
CC ASSOCIATION OF TWO DISULFIDE-LINKED HETERODIMERS; GENETIC FACTORS
CC DETERMINE WHICH OLIGOMER(S) WILL BE FORMED (STRAIN-SPECIFIC).
CC -1- PTM: N-GLYCOSYLATED; AT LEAST 3 OF THE POTENTIAL SITES ARE USED.
CC -1- TISSUE SPECIFICITY: KIDNEY, INTESTINAL BRUSH BORDERS, AND
CC SALIVARY DUCTS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC
CC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
CC -1- SIMILARITY: THE PROTEIN INCLUDES 1 EGF-LIKE REPEAT.
CC -1- SIMILARITY: CONTRAINS A MAM DOMAIN.
DR EMBL; M74897; M74897.
DR EMBL; M82962; M82962.
DR PIR; A40195; A40195.
DR PDB; 1IAF; 3I-AUG-94.
DR PROSITE; PS00142; ZINC_PROTEASE.
DR PROSITE; PS00740; MAM_
KM HYDROLASE; METALLOPROTEASE; ZINC; GLYCOPROTEIN; TRANSMEMBRANE;
KM ZMOGEN; SIGNAL; EGF-LIKE DOMAIN; 3D-STRUCTURE.
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CC		ANTIPARALLEL HETERODIMERS JOINED HEAD TO HEAD SO THAT EACH END
CC		OF THE NATIVE MOLECULE INCLUDES THE C-TERMINUS OF THE ALPHA
CC	-I-	SUBUNIT AND THE N-TERMINUS OF THE BETA SUBUNIT.
CC	-I-	SIMILARITY: TO ALPHA ACTININ AND DYSTROPHIN.
DR	EMLL M92288; M92288.	
DR	PIR; A33657; A33657.	
DR	PIR; A46147; A46147.	
DR	PDB; IDRO; PRELIMINARY.	
DR	FYBASE; FEGN0003471; SPEC-BETA.	
DR	PROSITE; PS00019; ACTININ_1.	
DR	PROSITE; PS00020; ACTININ_2.	
KM	CYTOSKELETON; MEMBRANE; CALMODULIN-BINDING; ACTIN-BINDING;	
KM	CAPPING PROTEIN; REPEAT; 3D-STRUCTURE.	
FT	REPEAT	36 268 1.
FT	REPEAT	269 379 2.
FT	REPEAT	380 494 3.
FT	REPEAT	495 605 4.
FT	REPEAT	606 711 5.
FT	REPEAT	712 ? 6.
FT	DOMAIN	2147 2259 PH.
SQ	SEQUENCE	2291 AA; 265785 MW; 18087143 CN;
Query Match		4.1%; Score 120; DB 7; Length 2291;
Best Local Similarity	21.7%;	Pred. No. 6,00e+03;
Matches	39; Conservative	36; Mismatches 53; Indels 13; Gaps 11;
Db	737 lenaveyfglfadddvdmldtlrlivsedvgvrdeanvsgllk-kh-kvadelpknya 794 : : : : : : : : : : : : : :	
Qy	134 LENLSEHLQIDANVEATGDLVDCTRPCE--SGEELALQHLYKKEKLIAQLDEKLRVFA 191	
Db	795 evdalshkqae-s-lkinea-eknavdk-plealdmrykeltelaktkrplldalsl-y 849 :: :: :: :: :: : : : :: : : :: : : : : :: :	
Qy	192 NIYAIVLKEVEDSHIALAASHQSGLDREHLLSLDERVELQQ-TIADQDVLTGLEHSL 250	
Db	850 klmsaa--dyvegw-ikektk 867 : :	
Qy	251 RLMEASFDGFITMKITNVTK 271	
RESULT	6	
ID	DYIS DROME STANDARD; PRT; 1319 AA.	
AC	P13496;	
DT	01-JAN-1990 (REL. 13, CREATED)	
DT	01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)	
DT	01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)	
DE	150 KD DYNEIN-ASSOCIATED POLYPEPTIDE (DP-150) (DAP-150) (GIUED PROTEIN).	
DE	GN GL.	
OS	DROSOPHILA MELANOCASTER (FRUIT FLY).	
OC	EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 87317680.	
RA	SMAROOP A.; SMAROOP W.; GAREN A.;	
RL	PROC. NATL. ACAD. SCI. U.S.A. 84:6501-6505(1987).	
CC	-I- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.	
CC	-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).	
CC	-I- SUBUNIT: CONSIST OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LOW MASS POLYPEPTIDES.	
CC	-I- SIMILARITY: CONTAINS A CAP-GU Y DOMAIN.	
CC	-I- SIMILARITY: STRONG, TO VERTEBRATE DYNACTIN.	

	DR	EMBL; J02933; J02932.
	DR	PfR_A28313; A28313.
	DR	FlyBASE; FBGN0001108; GL.
	DR	PROSITE; PS00845; CAP_GLY.
	KM	MOTOR PROTEIN; MICROTUBULES; DYNEIN; COILED COIL; CYTOSKELETON.
	FT	DOMAIN 2 19 SER-RICH.
	FT	DOMAIN 56 98 CAP-GLY.
	FT	DOMAIN 134 167 SER-RICH.
	FT	DOMAIN 255 564 COILED COIL.
	FT	DOMAIN 994 1124 COILED COIL.
SQ	SEQUENCE	1319 AA; 147858 MW; 8197543 CN;
	Query Match	3.8%; Score 115; DB 3; Length 1319;
	Best Local Similarity	25.0%; Pred. No. 2.65e-02;
	Matches 33; Conservative	35; Mismatches 58; Indels 6; Gaps 6;
Dc	426 lvrldrsahdhhtqlgklslemkrevevlerkekla-a-kidelaivadlqgyva	484
	: : : . : : : : : : : : :	
Oy	113 LAIVKEMKSPPGNSIAGAPMALENRLSEL-QLOAAVEATGDLEVDPYRAPCESOEIAL	171
Dc	465 a-lgaemveqaekkmledekvllseei-a-qleaevneqvvesnheldlire-e	540
	: : : : : : : : : : : : : :	
Oy	112 QHIVSKETLLAQLESKRVRPANIIVANIKREVASHLALASIHQSQUDEHHLSLEGRYVE	231
Dc	541 ldlangakkevl	552
	: : : :	
Oy	232 LQGTLAKRGVVL	243

DB	229	eggeelpeegtrgqpkyllegeegqlkhlheegglelpevgqpkhleql	288
0y	164	ESQELALDHLVKRKLIAQLLEKLRVFNATVAVLNR-EVESHSLALAASTHQ-S-QIDR-E	220

KM	SENSORY TRANSDUCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;
KW	TRANSMEMBRANE; INNER MEMBRANE; TRANSCRIPTION REGULATION.
FT	DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM 23 50 POTENTIAL.
FT	DOMAIN 51 57 PERIPLASMIC (POTENTIAL).
FT	TRANSSEM 58 77 POTENTIAL.
FT	DOMAIN 78 776 CYTOSOL PLASMIC (POTENTIAL).
FT	DOMAIN 269 515 TRANSMITTER DOMAIN (POTENTIAL).
FT	MOT RES 292 292 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CONFLICT 468 468 G -> GTG (IN REF. 1).
SQ	SEQUENCE 776 AA; 87824 MM; 3085590 CN;
 Query Match 3.6%; Score 105; DB 1; Length 776;	
Best Local Similarity 24.1%; Pred. No. 4,53e-01;	
Matches 21; Conservative 32; Mismatches 31; Indels 3; Gaps 3;	
Db	76 vvegleesqrqlarlgkyle-emterdlslvnglklmdaqnqelaavrekaaeletg 134
Qy	179 LLAQLLEKRLRFANVAIVLNKEVESHALLAASIHQSOLDREHLSTLRV-VELAQTLA 237
Db	135 qtkieikeetqdqleqgsfltrfll 161
Qy	238 Q-KDQVLAKLEHSIRLMEEASFDFGL 263
 RESULT 13	
ID	CENE HUMAN STANDARD; PRT; 2663 AA.
AC	Q02224;
DT	01-JUL-1993 (REL. 26, CREATED)
DT	01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE	CENTROMERIC PROTEIN E (CENP-E PROTEIN).
GN	CENP-E.
OR	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
NC	EUTHERIA; PRIMATES.
CC	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 93024922.
RA	YEN T.J., LI G., SCHAAER B.T., SELLAK I., CLEVELAND D.W.;
RL	NATURE 359:536-539(1992).
RN	[2]
RR	CHARACTERIZATION.
RX	MEDLINE; 95196755.
RA	THROWER D.A., JORDAN M.A., SCHAAER B.T., YEN T.J., WILSON L.;
RL	EMBO J. 14:918-926(1995).
CC	-1- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE
CC	KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
CC	OF THE CELL CYCLE. IMPORTANT FOR CHROMOSOME MOVEMENT
CC	AND/OR SPINDLE ELONGATION.
CC	-1- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC	CONDENSATION. RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC	QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC	-1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEINS FAMILY.
DR	EMI; 215005; 215005.
DR	PRI; S28261; S28261.
DR	MIM; 117143; 11TH EDITION.
DR	PROSITE; PS00411; KINESIN MOTOR DOMAIN.
KM	MOTOR PROTEIN; CELL DIVISION; ATP-BINDING; COILED COIL; MITOSIS;
KW	CELL CYCLE; CENTROMERE.
FT	DOMAIN 1 335 MECHANOCHEMICAL (MOTOR).
FT	DOMAIN 336 2471 COILED COIL (POTENTIAL).
FT	DOMAIN 2472 2663 GLOBULAR (POTENTIAL).
T1	NP_BIND 86 93 ATP (BY SIMILARITY).

Seq	SEQUENCE	2663 AA;	312087 MM;	23820152 CN;
Query Match		3.64;	Score 107;	DB 2;
Best Local Similarity		24.28;	Pred. No. 2.61e-01;	
Matches		22;	Conservative	28; Mismatches 37; Indels 4; Gaps 3;
Db	1773 gpeirihmhleqgeqidlqiyseektcklemqkdenaklqekiqelkanegql	1832		
Qy	166 GELTAQLQH-VKEKL--LAQLSEKRLRFANIVAVLNKEVESHSLAASIHQSQDLREHL	222		
Db	1833 itlkkdmetqkvsemeqkktqikdgsflil	1863		
Qy	223 LSLGRVVELQQTTLAQKQVLYKRL--ENSLAL	252		
RESULT	14			
ID	INVO CEBAL	STANDARD;	PRT;	428 AA.
AC	P24709;			
DT	01-MAR-1992 (REL. 21, CREATED)			
DT	01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)			
DT	01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)			
DE	INVOLUCRIN.			
OS	CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=ESOPHAGEAL FIBROBLAST;			
RX	MEDLINE; 92114750.			
RA	PHILLIPS M., RICE R.H., DUJAN P., GREEN H.;			
RL	MOL. BIOL. EVOL. 8:579-591 (1991).			
CC	- - FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS			
CC	IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO			
CC	MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE			
CC	FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.			
CC	- - TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND			
CC	OTHER STRATIFIED SQUAMOUS EPITHELIA.			
DR	EMBL; M67478; M67478.			
DR	PROSITE; PS00795; INVOLUCRIN.			
KM	KERATINOCYTE; REPEAT.			
SO	SEQUENCE	428 AA;	50126 MM;	809264 CN;
Query Match		3.58;	Score 102;	DB 4;
Best Local Similarity		34.88;	Pred. No. 1.02e+00;	
Matches		32;	Conservative	13; Mismatches 39; Indels 8; Gaps 8;
Db	207 eqeqgqlqepqvdqphhldqleqkqhpeqgeqkllleeeeqklhleqgeqkqhle	266		
Qy	164 ESQC-ELIALQHLHYE--KLLAQLEKTIATFANIVAVLNK--EVEASHLA--LAASIHQ--SQDL	218		
Db	267 qgeqglehlegqeqelkh--legceqglehleg	297		
Qy	219 R-E-HLISLEGRVVELQQTTLAQKQVLYKLEH	248		
RESULT	15			
ID	PC17 HUMAN	STANDARD;	PRT;	443 AA.
AC	O01850;			
DT	01-JUL-1993 (REL. 26, CREATED)			
DT	01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)			
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)			
DE	PARANEOPLASTIC CEREBELLAR DEGENERATION-ASSOCIATED ANTIGEN.			
DR	PCD17.			
OS	HOMO SAPIENS (HUMAN).			

SEQUENCE 443 AA; 50549 MM; 1032055 CN;

Matches 30; Conservative 30; Mismatches 44; Indels 11; Gaps 10;

Db 13 lqqlqlaelgkllldrntele-dsvqmytlngeqldeieyltkveillrqmneqhak 71

134 IERNIS-ELQ-ŲAAVEATGDIENVDCYRAPCCESQEEI-ALŲHIVKE-KILAQ-EEKIR 188

72 vyegj-dvtareleetnqklvadskasq-qk--ilsltetieclqtnidhlgsgv 122

189 VFANIVAVLNKEVEASHALAAISHQSLDREHLISLEQRVVELOQTAAQ-KDQV 242 QY

Job time : 16 secs.

Job time : 16 secs.

Dec 10 06:47

US-08-446-915-2.ppt

1

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:03:59 1996; MacPar time 17.22 Seconds

603.847 Million cell updates/sec

Tabular output not generated.

Title: >US-08-446-915-2

Description: (1-409) from US08446915.pep

Perfect Score: 2945

Sequence: 1 MASSSPADENEFQGCPPAD.....KAAVYKDDTMEKCIQVTSA 409

Scoring table: PAM 150

Gap 11

Searched: 82130 seqs, 25426960 residues

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database: p147

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unannc
14:unrev

Statistics: Mean 47.486; Variance 124.260; scale 0.382

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2589	87.9	416 11	B55649	TNFR-associated prot	0.00e+00
2	956	32.5	501 12	S56163	tumor necrosis facto	3.02e-125
3	794	27.0	568 11	A55649	TNFR-associated prot	9.73e-100
4	148	5.0	760 12	A40195	meprin A (EC 3.4.24.	6.60e-05
5	144	4.9	748 12	S24134	endopeptidase 2 (EC	1.57e-04
6	127	4.3	1048 3	BVECSC	sbcc protein - Esche	1.93e-05
7	120	4.1	2291 5	A46147	spectrin beta chain	8.87e-02
8	119	4.0	714 11	S39464	PABA peptide hydrola	1.13e-01
9	115	3.9	1319 10	A28313	glued protein - fru	2.96e-01
10	115	3.9	3259 11	S37536	macroglobulin - human	2.96e-01
11	111	3.8	3259 11	A56539	giantin - human	2.96e-01
12	111	3.8	700 11	S49383	meprin A (EC 3.4.24.	7.59e-01

Dec 10 06:47

US-08-446-915-2.ppt

2

13	112	3.8	870 3	GNMVA	pol polyprotein - sh	6.01e-01
14	113	3.8	1427 11	S26595	restin - human	4.75e-01
15	110	3.7	613 10	S27770	hypothetical protein	9.58e-01
16	106	3.6	601 11	S33377	p63 protein - human	2.40e+00
17	106	3.6	668 4	A42908	meprin A (EC 3.4.24.	2.40e+00
18	107	3.6	704 12	A48040	meprin beta chain pr	1.91e+00
19	105	3.6	778 3	RGECA	aerobic respiration	3.00e+00
20	105	3.6	1392 11	A43336	microtubule-vesicle	3.00e+00
21	107	3.6	2663 2	S28261	kinesin-related prot	1.91e+00
22	103	3.5	342 5	A24263	myosin heavy chain,	4.70e+00
23	104	3.5	385 5	C24263	myosin heavy chain,	3.76e+00
24	103	3.5	443 11	A49833	autoantigen recogniz	4.70e+00
25	103	3.5	467 1	UFEC	funarate hydratase (4.70e+00
26	103	3.5	509 11	A40448	DNA-binding protein	4.70e+00
27	104	3.5	582 10	S24545	intermediate filamen	3.76e+00
28	104	3.5	622 12	A57281	kinesin-like motor p	3.76e+00
29	104	3.5	622 12	S52487	CHO2 antigen - Chine	3.76e+00
30	104	3.5	741 10	A26572	bsg25D protein - fru	4.70e+00
31	103	3.5	872 3	TNBEH	97K alpha trans-indu	5.86e+00
32	102	3.5	1992 5	A47297	myosin heavy chain f	4.70e+00
33	103	3.5	2017 2	A36014	myosin heavy chain,	4.70e+00
34	100	3.4	92 7	S03214	hypothetical protein	9.09e+00
35	100	3.4	169 8	S03744	hypothetical protein	9.09e+00
36	101	3.4	567 3	RQECN	reol protein - Esche	7.31e+00
37	100	3.4	567 8	F64058	nitrate sensor prote	9.09e+00
38	101	3.4	738 9	A48246	ethylene-response pr	7.31e+00
39	101	3.4	917 7	S26365	P100 protein - Therm	7.31e+00
40	99	3.4	1053 11	A41642	dynactin - chicken	1.13e+01
41	100	3.4	1093 11	A47212	TAR element modulat	9.09e+00
42	100	3.4	1151 5	S09331	myosin beta heavy ch	9.09e+00
43	101	3.4	1325 14	S16129	dynein-associated pr	7.31e+00
44	101	3.4	1909 10	A45592	liver stage antigen	7.31e+00
45	99	3.4	2833 10	A43360	inositol 1,4,5-trisp	1.13e+01

ALIGNMENTS

RESULT 1
ENTRY B55649 #type complete
TITLE TNFR-associated protein EB16 - human
ORGANISM #formal name Homo sapiens #common name man
DATE 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 23-Mar-1995

ACCESSIONS B55649
REFERENCE A55649
#authors Mostafaei, G.; Birkenbach, M.; Yalamanchili, R.; VanReedale, T.; Ware, C.; Kleif, E.
#journal Cell (1995) 80:389-399

#title The Epstein-Barr virus transforming protein LMP1 engages
signaling proteins for the tumor necrosis factor receptor
family.
#accession B55649
#status preliminary
#molecule_type mRNA
#residues 1-416 #label MOS
#cross-references CB:019261

SUMMARY #length 416 #molecular-weight 46163 #checksum 6815

Query Match 87.9%; Score 2589; DB 11; Length 416;
Best local Similarity 84.4%; Pred. No. 0.00e+00;
Matches 345; Conservative 38; Mismatches 25; Indels 1; Gaps 1;
Db 8 sprpdpnefpgpvcqdkprralccaglsenprngdqickrcgldlslep 67
:::||||||| |||||: ||| ||| |||||:|||||:|:|||||:|||||:|

	FEATURE	#domain actaecin homology #label AST\
Dc	43-229 #domain MM homologous #label MAM	
SUMMARY	#length 714 #molecular-weight 80703 #checksum 3852	
	Query Match	4.0%; Score 119; DB 11; Length 714;
	Best Local Similarity 34.1%; Pred. No. 1.13e+01;	
Matches	29; Conservative 19; Mismatches 31; Indels 6; Gaps 6,	
Oy	403 vktvnrfs-gylent-skdsklqspfrfynse-gygfgvtlypnresagylrlia-fhvc-	457
	: : : - : - : : : : : : : : : : :	
Db	263 LKMTITVTKRCHESVCGRVTSLFSPAFYATKYGNTCLRLIYLNGDSSCKRHLSLFIVM	322
	:	
Oy	458 sgendailewpevrnryqtllidqe 482	
	: : : : : :	
Oy	323 RGEYDALPWFPRRK-VTFMLLDQN 346	
RESULT	9	AZ8313 #type complete
ENTRY	AZ8313	glued protein - fruit fly (<i>Drosophila melanogaster</i>)
TITLE	#formal name Drosophila melanogaster	
ORANISM	30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change	
DATE	31-Dec-1993	
ACCESSIONS	AZ8313	
REFERENCE	AZ8313	
#authors	Swatrop, A.; Swaroop, M.; Garten, A.	
#journal	Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6501-6505	
#title	Sequence analysis of the complete cDNA and encoded polypeptide for the glued gene of <i>Drosophila melanogaster</i> .	
#cross-references MOTID:	87317680	
#accession	AZ8313	
#molecule_type	DNA; mRNA	
#freelides	1-1319 ##label SMA	
#note	the authors' translation is inconsistent with the nucleotide sequence in the region 907-925	
GENETICS		
#introns	18/2; 479/3	
KEYWORDS	glycoprotein	
FEATURE		
	397,590,771,888, 980,1110,1127,1133, 1142	#binding site carbohydrate (Asn) (covalent) #status predicted
SUMMARY	#length 1319 #molecular-weight 147858 #checksum 8175	
	Query Match	3.9%; Score 115; DB 10; Length 1319; Best Local Similarity 25.0%; Pred. No. 2.96e-01;
Matches	33; Conservative 33; Mismatches 58; Indels 6; Gaps 6,	
Db	426 lwtlrldshndhdikqlklslemlkretevreletrekklas-kidealeivadiqqevda	484
	: : : : : : : : : : : : : : : :	
Oy	113 LAVIKEMSKPSGSNLKSAPMALERNLSEL-QIQAAVEATGDLVDYCVRAPCCSQEELAL	171
	:	
Db	465 a-lgaemveqkaekmelckvklldeeli-a-qleaeevhqdlevsnheledire-e	540
	: : : : : : : : : : : : : : :	
Oy	172 QHVLREKKLLAOLEEKLRPFANIIVAIWLAKKEVASHLTALAASIHQSQJDRHHLSLEQRIVE	231
	:	
Db	541 Idlangakevl 552	
	: : : : :	
Oy	232 LOOTLAOKDOVL 243	
RESULT	10	

[illegible]

[illegible]

KEYWORDS	endonuclease; hydrolase; nucleotidyltransferase; polyproteins; reverse transcriptase
SUMMARY	#length 870 #molecular-weight 99312 #checksum 4310
Query Match	3.8%; Score 112; DB 3; Length 870;
Best Local Similarity	24.7%; Pred. No.6.0e-01;
Matches 24; Conservative 27; Mismatches 42; Indels 4; Gaps 4;	
Dc	187 qlyvhydmlllahtcdhl-lyga-f-silkghslnglviadekigtbfpynglsfily 244 : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: Qy 166 ELAAGHVKKELIAQAQEKEIAVFANIVANLAKVEASHALAAASHQSUDREHL-LSLE 226 :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dc	245 prvyntqvlklqtch-lkrlnafdkllgdimwirpyl 280 :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Qy 227 QRVELAQOTLAQRKOVLGKLKHSIRIMEASFDGTFL 263	
RESULT 14	SZ2695 #type complete
ENTRY	restin - human
TITLE	#formal_name Hom sapiens #common_name man
ORGANISM	04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
DATE	18-Jun-1993
ACCESSIONS	SZ2695; S19853
REFERENCE	SZ2695
#authors	Bilbe, G.; Delabie, J.; Bruengen, J.; Richener, H.; Asselbergs, F.A.M.; Cerletti, N.; Sorg, C.; Odink, K.; Tarcsey, L.; Wiesendanger, W.; DeWolff-Peeters, C.; Shipman, R.
#journal	EMBO J. (1992) 11:2103-2113
#title	Restin: a novel intermediate filament-associated protein highly expressed in the Reed-Sternberg cells of Hodgkin's disease.
#cross-references	MUID:92289675
#accession	SZ2695
#molecule type	mRNA
#residues	1-1427 ##label BIL
#cross-references	EMBL:X64838
SUMMARY	#length 1427 #molecular-weight 160989 #checksum 428
Query Match	3.8%; Score 113; DB 11; Length 1427;
Best Local Similarity	25.0%; Pred. No.4.75e-01;
Matches 24; Conservative 31; Mismatches 34; Indels 7; Gaps 7;	
Dc	451 tkgdletqtkleharl-kelqasj-lfkctkdqlqreledrratvseksrimelekdl 508 : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: Qy 165 SQEELAIQ-HLVKEKLIQAQLEEKIARFANIVAV-LAKVEVASHLA-AAASHQSUDREH 221 :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dc	509 alrwge-vaelrrrl-esmkpqadvmslajleis 542 :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Qy 222 LSLERVELAQOTLAQRKOVLGKLKHSIRIMEAS 257	
RESULT 15	SZ7770 #type fragment
ENTRY	hypothetical protein I - African malaria mosquito (fragment)
TITLE	hypothetical Anopheles gambiae #common_name African malaria mosquito
ORGANISM	17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
DATE	18-Jun-1993
ACCESSIONS	SZ7770
REFERENCE	SZ7770
#authors	Bessansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Colline,

#submission submitted to the EMBL Data Library, June 1992

Accession	Submission	Description
U00000	submitted to the EMBL Data Library, June 1992	Distinct families of site-specific retroposons occupy identical positions in the rRNA genes of <i>Anopheles gambiae</i>

Accession S27770

molecule_type DNA

```
##Residues      1-613 ##Label BES
```

##cross-references EMBL:M93690

```
#length 613 #checksum 108
```

Query Match	Score	DB	Length
3.7%	110	10	613

Best Local Similarity 32.0%; Pred. No. 9.58e-01;

Matches 24; Conservative 17; Mismatches 31; Indels 3; Gaps 3;

Db 135 lseimeslklamqvajskelslcrkelgeslmknaalereletymrgarsvielqgga 194

Case	Age	Sex	Occupation	Duration of Illness	Onset	Course	Outcome
1	25	M	Teacher	10 years	1955	Chronic	Recovery
2	30	F	Homemaker	5 years	1960	Chronic	Recovery
3	35	M	Engineer	8 years	1958	Chronic	Recovery
4	40	F	Homemaker	12 years	1950	Chronic	Recovery
5	45	M	Teacher	15 years	1945	Chronic	Recovery
6	50	F	Homemaker	20 years	1940	Chronic	Recovery
7	55	M	Engineer	25 years	1935	Chronic	Recovery
8	60	F	Homemaker	30 years	1930	Chronic	Recovery
9	65	M	Teacher	35 years	1925	Chronic	Recovery
10	70	F	Homemaker	40 years	1920	Chronic	Recovery
11	75	M	Engineer	45 years	1915	Chronic	Recovery
12	80	F	Homemaker	50 years	1910	Chronic	Recovery
13	85	M	Teacher	55 years	1905	Chronic	Recovery
14	90	F	Homemaker	60 years	1900	Chronic	Recovery
15	95	M	Engineer	65 years	1895	Chronic	Recovery
16	100	F	Homemaker	70 years	1890	Chronic	Recovery
17	105	M	Teacher	75 years	1885	Chronic	Recovery
18	110	F	Homemaker	80 years	1880	Chronic	Recovery
19	115	M	Engineer	85 years	1875	Chronic	Recovery
20	120	F	Homemaker	90 years	1870	Chronic	Recovery

Qy 180 LAQLEEKLRVEANIVAVLNKEVASHALAAST-HQSQUDRE-HLISLEQR-VVEIQOTL 236

Db 195 aaapmtaqgahssr 209

Qy 237 A QKDVLGKLEHS LR 251

Search completed: Tue Dec 10 07:04:22 1996
Job time : 23 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:07:14 1996; MafPar time 20.07 Seconds

634.805 Million cell updates/sec

Tabular output not generated.

Title: >US-08-446-915-4
Description: (1-501) from US08446915.pep
Perfect Score: 3702
Sequence: 1 MAASVTSFGSELLQPEFS.....NSVWDADIFIKAVDITGL 501

Scoring table:

PAM 150
Gap 11

Searched: 82130 seqs, 25426960 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir47

1:am1 2:am2 3:am3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unannc
14:unrev

Statistics: Mean 48.057; Variance 117.898; scale 0.408

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	3770	88.3	501	12	S56163 tumor necrosis facto	0.00e+00
2	986	26.6	416	11	B55649 TNFR-associated prot	1.74e-138
3	806	21.8	568	11	A55649 TNFR-associated prot	3.03e-108
4	229	6.2	458	9	A29361 DC17 protein - sline	3.43e-16
5	162	4.4	700	11	S49383 meprin A (EC 3.4.24.	4.44e-07
6	162	4.4	760	12	A40195 meprin A (EC 3.4.24.	4.44e-07
7	158	4.3	487	3	DDBY18 DNA repair protein R	1.44e-06
8	158	4.3	704	12	A48040 meprin beta chain pr	1.44e-06
9	157	4.2	668	4	A42908 meprin A (EC 3.4.24.	1.93e-06
10	155	4.2	748	12	S24134 endopeptidase 2 (EC	3.45e-06
11	153	4.1	1483	3	RGBYH1 regulatory protein H	6.15e-06
12	153	4.1	1502	14	S59400 CYC1/CYP3 transcript	6.15e-06

13	141	3.8	377	11	A47380 RING finger-containi	1.86e-04
14	139	3.8	714	11	S39464 PABA peptide hydrola	3.24e-04
15	135	3.6	658	9	A44272 photomorphogenesis r	9.74e-04
16	126	3.4	336	11	S06573 finger protein (clon	1.10e-02
17	127	3.4	355	10	S57398 NIVA protein - Emeri	8.40e-03
18	127	3.4	443	10	S57328 uvw8 protein - Emeri	8.40e-03
19	127	3.4	477	10	S55494 C3H4 type zinc fing	8.40e-03
20	120	3.2	160	10	S28290 hypothetical protein	5.24e-02
21	119	3.2	227	5	S05585 tropomyosin - human	6.77e-02
22	119	3.2	596	10	S51157 intermediate filament	6.77e-02
23	120	3.2	1863	11	A54652 breast/ovarian cance	5.24e-02
24	114	3.1	284	11	S23470 beta-tropomyosin - A	2.40e-01
25	114	3.1	385	5	C24263 myosin heavy chain,	2.40e-01
26	113	3.1	400	7	S28022 outer membrane prote	3.08e-01
27	114	3.1	501	14	S34825 uvw2 protein - Neuro	2.40e-01
28	110	3.0	529	11	S06565 finger protein (clon	6.45e-01
29	110	3.0	675	11	S51037 zinc-finger protein	6.45e-01
30	112	3.0	1042	12	S42511 RAG-1 protein - rabb	3.94e-01
31	112	3.0	1042	12	S44379 RAG-1 protein - rabb	3.94e-01
32	111	3.0	1043	12	B33754 recombination-activa	5.05e-01
33	110	3.0	1043	11	A33754 recombination-activa	6.45e-01
34	111	3.0	1992	5	A47297 myosin heavy chain f	5.05e-01
35	107	2.9	321	11	D39371 Ig V-region-like B-g	1.33e+00
36	109	2.9	393	12	JN0533 finger protein pML2-	8.23e-01
37	107	2.9	406	14	S59296 probable Zn-finger (1.33e+00
38	106	2.9	458	5	S09228 intermediate filament	1.65e+00
39	107	2.9	879	5	S20486 paramyosin - fruit f	1.33e+00
40	107	2.9	879	5	S20208 paramyosin, standard	1.33e+00
41	104	2.8	284	2	TWCHS1 tropomyosin 1, smoot	2.72e+00
42	104	2.8	458	5	A43549 vimentin 1 - African	2.72e+00
43	105	2.8	463	5	B43549 vimentin 4 - African	2.15e+00
44	104	2.8	624	11	S28418 probable zinc-bindin	2.72e+00
45	104	2.8	2094	11	S33124 tpr protein - human	2.72e+00

ALIGNMENTS

RESULT	1	
ENTRY	S56163	#type complete
TITLE	tumor necrosis factor receptor-associated protein - human	
ALTERNATE_NAMES	TNF receptor-associated protein	
ORGANISM	#formal name Homo sapiens #common name man	
DATE	10-Oct-1995 #sequence_revision 01-Dec-1995 #text_change 01-Dec-1995	
ACCESSIONS	S56163; S58925; S58926	
REFERENCE	S56163	
##authors	Song, H.Y.; Donner, D.B.	
##journal	Biochem. J. (1995) 309:725-879	
##title	Association of a RING finger protein with the cytoplasmic domain of the human type-2 tumour necrosis factor receptor.	
##accession	S56163	
##molecule_type	mRNA	
##residues	1-501 ##label SON	
##cross-references	EMBL:012597	
REFERENCE	S58925	
##authors	Song, H.Y.; Donner, D.	
##submission	submitted to the EMBL Data Library, July 1994	
##description	Association of a RING finger protein with the cytoplasmic domain of the human type 2 TNF receptor.	
##accession	S58925	
##molecule_type	mRNA	
##residues	1-42,63-342,363-501 ##label SON	
##cross-references	EMBL:012597	
##accession	S58926	


```
##molecule type mRNA
##residues 1-342, RPEOAGCGHRYCSFCLASIL, 363-501 ##label SOE_
##cross-references EMBL:U12597
KEYWORDS
zinc finger
SUMMARY
#length 501 #molecular-weight 55842 #checksum 5395
```

Query Match	88.3%;	Score 3270;	DB 12;	Length 501;
Best Local Similarity	86.6%;	Pred. No. 0.00e+00;		
Matches 434;	Conservative 36;	Mismatches 31;	Indels 0;	Gaps 0;

Db	1	maasvnpopslellqogfcklljgtkleeakjleacnmvllrrpbgdqchyscfac	60
Qy	1	MAASVNPSPSLELLQOPFSKTLCTGTRLEKYLCSACKNLIRRPQAOQCHRCSCFLTS	60
Db	61	llsaspncaacvchqyveeqglellsnessfmdaarreveslpavpsdqctwkgtlke	120
Qy	61	llsaspncaacvchqyveeqglellsnessfmdaarreveslpavpsdqctwkgtlke	120
Db	121	yeechegrcplmtcepackqvlrjgekerhlehceperleschracpcgadkahlhe	180
Qy	121	YESCHEGRCPLMTCEPACKGVLRJGEKERHLEHCEPERLESCHRCAPCSHVDKHAHE	180
Db	181	vcpkfpilcdgqcgkkliprekfghvktcgcrcvpcfhajgclevegeqgehevaj	240
Qy	181	VCPKFPILCDGCGKKLIPREKFGHVKTCCRCVPCFHAJGCLVEVEGEQGEHEVAJ	240
Db	241	rehlamllsaevlaekprrlggdqshassellbrceslekkattefemvcevhnevavama	300
Qy	241	REHLALLSSFLEMAASPGTLQVOPREHLRQOQLEDRKATFENIVCEVILNREVERAVAMA	300
Db	301	eacscphridqckleialeakvvgqleerisgikclamaadeqkvelmeasdydvfwkisd	360
Qy	301	EACSCPHRIDQCKTLEALSNNVQOLESRTGLKDLAMADEQKSELEVSVDGVFWKISD	360
Db	361	fprcklgeavagrtipaisfasyfstergykmclrlvngdqtgrqtblhlfvwmkypnda	420
Qy	361	FPRCKQGEAVAGRTIPASFAFYSYSGYKMCRLVYVNGDQGTGRGTHLSLFVWVMKGND	420
Db	421	llrwpfngkvrtlmllldqmrnehvldafpdrtsesfprvpmndiaaegcpilcpvskmea	480
Qy	421	LLRWPFGNKVRTLMLLDNNRNEHVLDARPRDYTSSSFRPVSDMNTIASGPIFCPVSKME	480
Db	481	knsyvrdcaifikaivdtlgl	501
Qy	481	KNSYVRDCAIFIKAVDVTGL	501

RESULT	2	
ENTRY	B55649	#type complete
TITLE	TNFR-associated protein EB16 - human	
ORGANISM	#formal name Homo sapiens #common name man	
DATE	23-Mar-1995	#sequence_revision 23-Mar-1995 #text_change 23-Mar-1995
ACCESSIONS	B55649	
REFERENCE	A55649	
#authors	Mosialoe, G.; Birkenbach, M.; Yalamanchili, R.; Vamvakisdale, T.; Ware, C.; Kleff, E.	
#journal	Cell (1995) 80:389-399	
#title	The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family.	
#accession	B55649	
#status	preliminary	
#molecule_type	mRNA	

```
##residues      1-416 ##label MOS
##cross-references GB:U19261
SUMMARY      #length 416 #molecular-weight 46163 #checksums 6815
```

Query Match	26.6%	Score 986	DB 11	Length 416
Best Local Similarity	55.4%	Pred. No. 1,74e-138		
Matches 124	Conservative	59	Mismatches 40	Indels 1
			Gaps	1

[illegible]

ENTRY	3	RESULT
TITLE	A55649	#type complete
ALTERNATE_NAMES	TNFR-associated protein LMP1 - human	
ORGANISM	CD40-binding protein	
DATE	#formal_name Homo sapiens #common_name man	
	23-Mar-1995 #sequence_revision 23-Mar-1995	#text_change
	05-Apr-1995	
ACCESSIONS	A55649; A55135	
REFERENCE	A55649	
#authors	Mostoslav, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.	
#journal	Cell (1995) 80:389-399	
#title	The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family.	

```

#accession      A53649
##molecule_type mRNA
##residues      1-568 ##label MOS
##cross-references GB:U19260
##note          nucleotide sequence not given
REFERENCE
A53135
#authors        Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.
#journal         J. Biol. Chem. (1994) 269:30669-30072
#title          A novel RING finger protein interacts with the cytoplasmic
                domain of CD40.
                domain of CD40.
#accession      A53135
##molecule_type mRNA
##residues      1-133, 135-404, 'G', 406-568 ##label HDA
##cross-references GB:U15637
##note          nucleotide sequence not given
                coiled coil
KEYWORDS
FEATURe        #region RING-finger motif
53-91
SUMMARY        #length 568 #molecular-weight 64490 #checksum 8660

```

53-91	#region	RING-finger motif	
SUMMARY	#length	568	#molecular-weight 64490
			#checksum 8660
Query Match	21.8%	Score 806; DB 11;	length 568;
Best Local Similarity	52.7%;	Pred. No. 3,036-108;	
Matches	98;	Conservative	50;
		Mismatches	36;
		Indels	2;
		Gaps	2

[illegible]

RESULT	4	
ENTRY	A29361	#type complete
TITLE	Dc17 protein - slime mold (Dictyostellium discoideum)	
ORGANISM	#formal_name Dictyostellium discoideum	
DATE	31-Mar-1989 #sequence_revision 31-Mar-1989	#text_change 31-Dec-1993
ACCESSIONS	A29361	
REFERENCE	A29361	
#authors	Driscoll, D.M.; Williams, J.G.	
#journal	Mol. Cell. Biol. (1987) 7:4482-4489	
#title	Two divergently transcribed genes of Dictyostellium discoideum are cyclic AMP-inducible and coregulated during development.	
#cross-references	NCBI:88142840	
#accession	A29361	
#molecule_type	DNA	
#residues	1-458	#label DRI
KEYWORDS	DNA binding; zinc finger	
SUMMARY	#length 458 #molecular_weight 53015	#checksum 3923

	Query Match	6.2%	Score 229,	DB 9,	Length 458;
	Best Local Similarity	24.8%;	Pred.	No.3,43e-16;	
	Matches	64;	Conservative	68;	Mismatches 103;
				Indels	23; Gaps
Dd	79 clawetadfkcecc-clty-s-fneqivegtctscppdgasvqrnllkd-eengckeki	134			
	: : : : : : : : : :				
Qy	57 CLTSLISGPGNCACAYEGIALEGISLILESSAFPNMARREVESIPAVCPNDGCWKG	116			
Dd	135 evdqids-nlincgkftvcsf-kycekil-rmslxmngfvlvtcdcfckrdclkkkel	191			
	: : : : : : : : : : : : :				
Qy	117 TLKEVSESGHEGLPFLTECPRKGLWLRLSEKHHTGTGEOPKRSLSCGH-C-RAPCSHDL	175			
Dd	192 ethyticpmvpidecsgcsvk-lertkailldhendcntqipoky feegckveamkrse-l	249			
	: : : : : : : : : : :				
Qy	176 EYMEVECKRPFLTC-DGGKKRIETREFPDNH-RACSKGVLCERHYTGGS-EMATEENL	232			
Dd	250 qnh-lervnqhnygmjlliek-ltnvgqsckth-d-elikkiedslilvikfed-ac-lk	303			
	: : : : : : : : : : : :				
Qy	233 QDNEIDRLRHH-LALLLSFLEAASPGTLNQVPELLDRQILLKRIATFNIVCVIN	290			
Dd	304 kvw--lpkaldicengyr	319			
	:: : : : : : : : : : :				
Qy	291 REVERVAVTAECSRGHR	308			

RESULT	5	
ENTRY	S49383	#type complete

TITLE	meprin A (EC 3.4.24.18) - human
ORGANISM	#formal name Homo sapiens #common name man
DATE	16-Feb-1995 #sequence_revision 12-May-1995 #text_change 26-May-1995
ACCESSIONS	S49383
REFERENCE	S49383
#authors	Eldering, J.A.; Greenberg, J.; Sterchi, E.E.
#submission	submitted to the EMBL Data Library, September 1994
#description	Cloning and the PABA-peptide hydrolase beta subunit: compression is required for plasma membrane localization of the alpha subunit in COS-1 cells.
#accession	S49383
#status	preliminary
#molecule_type	mRNA
#residues	1-700 #label ELD
#cross-references	EMBL:X81333
CLASSIFICATION	#superfamily MM homology; astacin homology
FEATURE	
71-257	#domain astacin homology #label ASTV
260-429	#domain MM homology #label MM
SUMMARY	#length 700 #molecular-weight 19458 #checksum 916
Query Match	4.4%; Score 162; DB 11; Length 700;
Best Local Similarity	33.3%; Pred. No. 4,44e-07;
Matches	35; Conservative 33; Mismatches 22; Indels 15; Gaps 11;
Db	431 lwlnrft---q-figsngnqlsyppfysak-gy-a-fqilyn--lahvtnagiylfi 480
Qy	355 IWKISDFTKRGQEAVALRPALFSPATYSRYCYKMGCLARYLNGDGRGTHLSLFVVM 414
Db	481 sganddlqwpowpqqatmlldgmpldqrmnq-rs-ittdpf 523
Qy	415 KGRVDALLQMEFN-QKVTMLMLDNN-N-REHYTDARFPDYTSSTF 456
RESULT	6
ENTRY	AA0195 #type complete
TITLE	meprin A (EC 3.4.24.18) alpha chain precursor - mouse
ALTERNATE_NAMES	endopeptidase-2
ORGANISM	#formal_name Mus musculus #common name house mouse
DATE	16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 23-Mar-1995
ACCESSIONS	AA0195; BA1196
REFERENCE	AA0195
#authors	Jiang, W.; Gorbea, C.M.; Flannery, A.V.; Beynon, R.J.; Grant, G.A.; Bond, J.S.
#journal	J. Biol. Chem. (1992) 267:9185-9193
#title	The alpha subunit of meprin A. Molecular cloning and sequencing, differential expression in inbred mouse strains, and evidence for divergent evolution of the alpha and beta subunits.
#cross-references	MUID:92250517
#accession	AA0195
#molecule_type	mRNA
#residues	1-760 #label JIA
#cross-references	GB:M74897
#note	part of this sequence, including the amino end of the mature protein, was confirmed by protein sequencing
REFERENCE	AA1196
#authors	Dummermuth, E.; Sterchi, E.E.; Jiang, W.; Wolz, R.L.; Bond, J.S.; Flannery, A.V.; Beynon, R.J.
#journal	J. Biol. Chem. (1991) 266:21381-21385
#title	The astacin family of metalloendopeptidases.
#cross-references	MUID:92042028

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#accession	B41196
##molecule_type	mRNA
##residues	77-275 ##label DUM
##cross-references	CB:M74897; CB:M74238
CLASSIFICATION	#superfamily ascacin homology; MAM homology
FEATURE	
1-33	#domain signal sequence #status predicted #label SIG\
34-77	#domain propeptide #status predicted #label PRO\
78-760	#product mepirin A alpha chain #status experimental #label MAT\
87-273	#domain astracin homology #label AST\
276-445	#domain MAM homology #label MAM
SUMMARY	#length 760 #molecular-weight 85702 #checksum 4733
Query Match	4.4%; Score 162; DB 12; Length 760;
Best Local Similarity	32.9%; Pred. No. 4,44e-07;
Matches	28; Conservative 25; Mismatches 28; Indels 4; Gaps 6
Db	447 vntirmisqilentvkgdk-lv-spr-fynse-gygygvtltpngritsnslglftfhy 503
Oy	355 IKMISDFRKQGAVAGCRPAITSPFAFTSNYGKMKCLRYVIAMDGTGRCHLSLFFVM 414
Db	504 sgdnadallwpenrgatmlldge 528
Oy	415 KCPNDALLQPFNQKVTLH-LLDHN 438
RESULT	7
ENTRY	DOB718 #type complete
TITLE	DNA repair protein RAD18 - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES	protein YC8066*
ORGANISM	#formal_name Saccharomyces cerevisiae
DATE	31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-May-1995
ACCESSIONS	S05802; S22263; S19481; JS0082
REFERENCE	
#authors	Jones, J.S.; Weber, S.; Prakash, L.
#journal	Nucleic Acids Res. (1988) 16:7119-7131
#title	The Saccharomyces cerevisiae RAD18 gene encodes a protein that contains potential zinc finger domains for nucleic acid binding and a putative nucleotide binding sequence.
#cross-references	MUID:8630333
#accession	S05802
##molecule_type	DNA
##residues	1-487 ##label JON
##cross-references	EMBL:X12588
REFERENCE	
#authors	Benit, P.; Chanet, R.; Fabre, F.; Faye, G.; Fukuhara, H.; Sor, F.
#journal	Yeast (1992) 8:147-153
#title	Sequence of the sup61-RAD18 region on chromosome III of Saccharomyces cerevisiae.
#cross-references	MUID:92221691
#accession	S22263
##molecule_type	DNA
##residues	1-487 ##label BEN
##cross-references	EMBL:S93198
REFERENCE	
#authors	Antoine, G.; Benit, P.; Chanet, R.; Fabre, R.; Faye, G.; Fukuhara, H.; Mathieu, A.; Sor, F.
#submission	submitted to the Protein Sequence Database, March 1992
#accession	S19481
##molecule_type	DNA
##residues	1-487 ##label ANT

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US-08-446-915-4.rpt

88

```

#cross-references EMBL:X59720
REFERENCE JS0082
#authors Chanet, R.; Magana-Schwencke, N.; Fabre, F.
#journal Gene (1988) 74:543-547
#title Potential DNA-binding domains in the RAD18 gene product of
Saccharomyces cerevisiae.
#cross-references MUID:8932745
accession JS0082
#molecule_type DNA
#residues 1-487 ##label CHA

GENETICS
#gene LISTA:RAD18
#map_position 3R
CLASSIFICATION #superfamily DNA repair protein RAD18
KEYWORDS ATP; DNA binding; DNA repair; zinc finger
FEATURE
#region zinc finger motif
51-65 #region zinc finger motif\
190-210 #region zinc finger motif\
366 #binding_site ATP (lys) #status predicted
SUMMARY #length 487 #molecular_weight 55230 #checksum 1135

Query Match 4.3%; Score 158; DB 3; Length 487;
Best Local Similarity 36.7%; Pred. No.1,44e-06;
Matches 18; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

Db 21 qdltlrchickdfkxpvtpqgctscicrtlhmp-npclelle 68
::: | ::::: | : ||| ::::: | : | | ::::: | : |
QY 27 RLKAYLCACGKNILRRPQAGCHRCVCELTSLISGPNACACVE 75

RESULT 8
ENTRY A48040 #type complete
TITLE meprin beta chain precursor - mouse
ORGANISM #formal_name Mus musculus; #common_name house mouse
DATE 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change
07-Jul-1995

ACCESSIONS A48040
REFERENCE A48040
#authors Gorbea, C.M.; Marchand, P.; Jiang, W.; Copeland, N.G.;
Gilbert, D.J.; Jenkins, N.A.; Bond, J.S.
J. Biol. Chem. (1993) 268:21035-21043
#journal Cloning, expression, and chromosomal localization of the
#title mouse meprin beta subunit.
#accession A48040
#status preliminary
#molecule_type mRNA
#residues 1-704 ##label GOR
##cross-references GB:L15193
CLASSIFICATION #superfamily MM homology; astacin homology
FEATURE
72-258 #domain astacin homology #label AST\
261-430 #domain MM homology #label MM
SUMMARY #length 704 #molecular_weight 79585 #checksum 7013

Query Match 4.3%; Score 158; DB 12; Length 704;
Best Local Similarity 32.7%; Pred. No.1,44e-06;
Matches 34; Conservative 34; Mismatches 22; Indels 14; Gaps 11;

Db 432 lwhqfnt---q-ilggqtvsyppfsysk-gy-a-fqlym--dlr-ystngvlyfnli 481
|||::| | ::::: ||::: ||| ::::: | : | | ::::: | : |
QY 355 IWKTSFTRKRGEAVGRPAIFSPAFYSRYGYKMCLRVYINAGDGTGRGHLSLFYVM 414

Db 482 sgandqlgwpcwqgatnlldqnpdiqrgrmfng-tsiltcptc 524
```


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18-NOV-1994

ACCESSIONS	A44272
REFERENCE	A44272

#authors

Feldmann, K.A.; Quail, P.H.

#journal
#title
Cell (1992) 71:791-801
COP1, an Arabidopsis regulatory gene, encodes a protein with

both a zinc-binding motif and a G beta homologous domain.
#cross-references MUID:93046683

#contents	Columbia ecotype
#accession	A44272

```
##status      preliminary; not compared with conceptual translation
##molecule type nucleic acid
```

```
##residues      1-658 ##label DEN
```

```
##cross-references NCBI:118657
##note
sequence extracted from NCBI backbone
```

SUMMARY #length 658 #molecular-weight 74568 #checksum 7029

Query Match	3.6%; Score 135; DB 9; length 658;
-------------	------------------------------------

Best Local Similarity	31.1%;	Pred. No. 9.74e-04;
Matches	14; Conservative	14; Mismatches 16; Indels 1; Gaps 1;

Db 46 ldkdlcpcmqiklkdafltaqhsfcymciithlrns-dcpc 89

Qy 28 LEAKYCSACKNILRRPFQAOQCHRYCSFCLTSLSSGPQNCAC 72

Search completed: Tue Dec 10 07:08:25 1996
Job time : 71 secs.

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MPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:06:29 1996; MasPar time 13.19 Seconds

660,452 Million cell updates/sec

Tabular output not generated.

Title: >US-08-446-915-4
Description: (1-501) from US08446915.pep
Perfect Score: 3702

Sequence: 1 MAASVTPSGSELLQPGFS.....NSTYRDALFIKAVLDLTGL 501

Scoring table:
PAM 150
Gap 11

Searched: 49340 seqs, 17385503 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9

Statistics: Mean 50.182; Variance 93.568; scale 0.536

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
	1	3702	100.0	501	8	TNF2_MOUSE	TNF RECEPTOR ASSOCIAT	0.00e+00
	2	3702	26.3	409	8	TNF1_MOUSE	TNF RECEPTOR ASSOCIAT	1.75e-178
	3	229	6.2	458	2	DG17_DICD1	DG17 PROTEIN.	1.30e-21
	4	162	4.4	760	5	MEPA_MOUSE	MEPRIN A ALPHA-SUBUNIT	7.47e-10
	5	158	4.3	487	6	RA18_YEAST	DNA REPAIR PROTEIN RA	3.37e-09
	6	157	4.2	668	5	MEPB_RAT	MEPRIN A BETA-SUBUNIT	4.90e-09
	7	153	4.1	1483	2	CYP1_YEAST	CYP1 ACTIVATORY PROTE	2.17e-08
	8	141	3.8	377	7	RINI_HUMAN	RING1 PROTEIN.	1.69e-06
	9	135	3.6	675	2	COP1_ARATH	COP1 REGULATORY PROTE	1.40e-05
	10	126	3.4	647	9	ZG48_XENLA	GASTRULA ZINC FINGER	3.04e-04
	11	120	3.2	160	9	YNN1_CAEEL	HYPOTHETICAL 18.7 KD	2.21e-03
	12	119	3.2	227	8	TPMS_HUMAN	TROPOMYOSIN ALPHA CHA	3.06e-03
	13	120	3.2	1863	1	BRC1_HUMAN	BREAST CANCER TYPE 1	2.21e-03

14	113	3.1	400	6	OMPA_THEMA	OUTER MEMBRANE PROTEI	2.07e-02
15	114	3.1	501	8	UVS2_NEUCR	UVS-2 PROTEIN.	1.51e-02
16	110	3.0	529	8	ZG20_XENLA	GASTRULA ZINC FINGER	5.24e-02
17	111	3.0	1040	7	RAG1_MOUSE	V(D)J RECOMBINATION A	3.85e-02
18	112	3.0	1042	7	RAG1_RABIT	V(D)J RECOMBINATION A	2.82e-02
19	110	3.0	1043	7	RAG1_HUMAN	V(D)J RECOMBINATION A	5.24e-02
20	106	2.9	389	5	MYSP_SCHUA	PARAMYOSIN (FRAGMENT)	1.76e-01
21	109	2.9	393	5	ML24_MOUSE	PARAMYOSIN BETA 3, F	7.12e-02
22	106	2.9	458	4	IE3T_TORCA	TYPE III INTERMEDIATE	1.76e-01
23	107	2.9	879	5	MYSP_DROME	PARAMYOSIN, LONG FORM	1.31e-01
24	104	2.8	248	8	TPM3_CHICK	TROPOMYOSIN ALPHA 3, F	3.19e-01
25	104	2.8	284	8	TPM1_HUMAN	TROPOMYOSIN ALPHA CHA	3.19e-01
26	104	2.8	284	8	TPM1_CHICK	TROPOMYOSIN 1, SMOOTH	3.19e-01
27	103	2.8	284	8	TPMB_CHICK	TROPOMYOSIN BETA CHAI	4.28e-01
28	102	2.8	284	8	TPM1_CLOIN	TROPOMYOSIN, SMOOTH M	5.73e-01
29	104	2.8	309	5	MYSA_MESNU	MYOSIN HEAVY CHAIN, C	3.19e-01
30	102	2.8	430	1	AROA_STRAU	3-PHOSPHOSHIKIMATE 1-	5.72e-01
31	104	2.8	458	8	VIMI_XENLA	VIMENTIN 1 AND 2.	3.19e-01
32	105	2.8	463	8	VIM4_XENLA	VIMENTIN 4.	2.37e-01
33	104	2.8	624	1	A33_PLENA	ZINC-BINDING PROTEIN	3.19e-01
34	105	2.8	648	2	CH44_YEAST	CH44 ACTIVATORY PROTE	2.37e-01
35	102	2.8	811	4	HSP7_YEAST	MITOCHONDRIAL HEAT SH	5.73e-01
36	102	2.8	1959	5	MYSN_CHICK	MYOSIN HEAVY CHAIN, N	5.73e-01
37	101	2.7	284	8	TPMB_RABIT	TROPOMYOSIN BETA CHAI	7.64e-01
38	101	2.7	284	8	TPMB_HUMAN	TROPOMYOSIN BETA CHAI	7.64e-01
39	100	2.7	284	8	TPMA_XENLA	TROPOMYOSIN ALPHA CHA	1.02e+00
40	101	2.7	337	9	ZG26_XENLA	GASTRULA ZINC FINGER	7.64e-01
41	101	2.7	403	4	KICS_MOUSE	KERATIN, TYPE I CYTOS	7.64e-01
42	101	2.7	454	8	TNR1_MOUSE	TUMOR NECROSIS FACTOR	7.64e-01
43	101	2.7	465	8	VIME_HUMAN	VIMENTIN.	7.64e-01
44	101	2.7	1314	1	ADR6_YEAST	TRANSCRIPTION FACTOR	7.64e-01
45	101	2.7	1978	5	MYSG_CHICK	MYOSIN HEAVY CHAIN, G	7.64e-01

ALIGNMENTS

ID	TRF2_MOUSE	STANDARD;	PRT;	501 AA.
AC	P39429;			
DT	01-FEB-1995 (REL. 31, CREATED)			
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)			
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)			
DE	TNF RECEPTOR ASSOCIATED FACTOR 2 (TNFA2).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 94349371.			
RA	ROTHE M., WONG S.C., HENZEL W.J., GOEDEDEL D.V.;			
RL	CELL 78:681-692(1994).			
CC	-1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN			
CC	OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.			
CC	-1- SIMILARITY: CONTRAINS A C3HC4-CLASS ZINC FINGER.			
DR	EMBL; L35303; L35303.			
DR	PROSITE; PS00518; ZINC_FINGER_C3HC4.			
KM	ZINC_FINGER; COILED COIL.			
FT	ZN FING 34 72 C3HC4-TYPE.			
SQ	SEQUENCE 501 AA; 56026 MW; 1264825 CN;			
Query Match	100.0%; Score 3702; DB 8; Length 501;			
Best Local Similarity	100.0%; Pred. No. 0.00e+00;			

Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D	b	1	maasvtrpgselrlpqfsakrlglgttleakyjcsacknllrpfqacqhyrcsfcls	60
Q	y	1	MAASVTPGSELRLPGFSKTLGLTRLEAKYLCACKNLLRPFQACGHRYSCLFLS	60
D	b	61	ilsagpmcaacryeqylveegisilsleesaeafpdaarveeslpavcndqctwqylke	120
Q	y	61	ILSGPMCAACYEGYELVEEGISTLESSEAFPDNARREVSIPAVCNDQCTWQYLTKE	120
D	b	121	yesheqjlcpfllllepackqlvrlsekehhegecprelsedqctrapcshvdehve	180
Q	y	121	YESCHEGJLCPFLLLLEPACKQLVRLSEKHHGECPRELSLSDQCTRAPCSHVDLVHVE	180
D	b	181	vcpbfrlpcdcqgkklkprctfqdhvrascaervlcrfhvcgseavetelnqdhelqr	240
Q	y	181	VCPBFRPCDCQGKLLKPRCTFQDHRVASCARVLCRFHVCGSEAVETELNDHELQRL	240
D	b	241	rehlallllesflaesagpvtlmgvpejlqrcqjleokiatfeniwcvlneveravtra	300
Q	y	241	REHLALLLSFLLEASAGPVTLMGVPEJLQRCQJLEOKIATFENIWCVLNEVERAVTRA	300
D	b	301	eacsrqtrhltdqkileaslnkvqgderisrlgkllamadlseqvselevestydygrfikisd	360
Q	y	301	EACSRQTRHLDQKILEASLNKVQGLDERISRLGKLLAMADLSEQVSELEVSTYDYGRFIKISD	360
D	b	361	ftckrqeavagtrpalfspafyterarygkmcrlrylngdqtgrghlsiffvmvxpnda	420
Q	y	361	FTCKRQEAVAGTRPALFSPAFYTERARYGKMCRLRYLNGDQTRGHLSLFFVMVXPND	420
D	b	421	llqwpfngkvtlmalldhnnrehvldafpdrtssefqrpvsdmniaasgcpilfcovpkeaa	480
Q	y	421	LLQWPFNGKVTLMALLDHNNREHVLDARPDRTSSSFQRPVSDMNIAASGCPILFCOVSKEEA	480
D	b	481	kneyvrdafefikaivdlcql	501
Q	y	481	KNEYVRDAFEFIKAIVDLCQL	501

ID	TRF1 MOUSE	STANDARD	PRT	409 AA.
AC	P39428;			
DT	01-FEB-1995 (REL. 31, CREATED)			
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)			
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)			
DE	TNF RECEPTOR ASSOCIATED FACTOR 1 (TRAF1).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUMAROTEA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
NC	EUTHERIA; RODENTIA.			
LN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND 390-402.			
RP	MEDLINE; 94349371.			
RA	ROTHE M., WONG S.C., HENZEL W.J., GOEDEL D.V.;			
RL	CELL. 78:681-692(1994).			
CC	-1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN			
CC	OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- SUBUNIT: HETERODIMER OF TRAF1 AND TRAF2.			
DR	EMBL; L35302; L35302.			
KM	COILED COIL.			
SQ	SEQUENCE 409 AA; 45464 MW; 857796 CN;			

Query Match	26.3%;	Score 972;	DB 8;	Length 409;
Best Local Similarity	54.0%;	Pred. No. 1.75e-178;		

Matches 121; Conservative 61; Mismatches 41; Indels 1; Gaps 1;

[illegible]

RESULT	3	STANDARD	PRT	458 AA.
ID	DG17 DICI			
AC	P11467			
DT	01-OCT-1989 (REL. 12, CREATED)			
DT	01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	DG17 PROTEIN.			
GN	ZFAA OR DG17.			
OS	DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).			
OC	EUKARYOTA; PROTOZOA; SARCOMASTICOPHORA; SARCODINA; RHIZOPODA;			
CC	EUMLCETOZA; DICTYOSTELIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 88142840.			
RA	DRISCOLL D.M., WILLIAMS J.G.;			
RL	MOL. CELL. BIOL. 7:4482-4489(1987).			
CC	-1- THE EXPRESSION OF DG17 PROTEIN IS DEVELOPMENTALLY REGULATED			
CC	-1- INDUCTION. BY CAMP DURING AGGREGATION.			
DR	EMBL; M18106; M18106.			
DR	PIR; A29361; A29361.			
DR	DICTYDB; DD02010; ZFAA.			
KM	DEVELOPMENTAL PROTEIN; ZINC-FINGER.			
FT	SIMILAR 25 67 TO DR05OPHILIA SINA (AA 71-108).			
FT	ZN_FING 27 66 POTENTIAL.			
FT	ZN_FING 178 198 POTENTIAL.			
FT	SEQUENCE 458 AA; 53015 MW; 1107348 CU;			
50				

Query Match 6.2%; Score 229; DB 2; Length 458;
Best Local Similarity 24.8%; Pred. No. 1.30e-21;
Matches 64; Conservative 68; Mismatches 103; Indels 23; Gaps 22.

Db 79 clverafckkacc-cly-s-ineqiveggicppdgaavqgnllkd-geongcexki 134
 Qy 57 cltjtsllssopocnaecygcleglvegisillesssapPnnaArRevStPAPCPDCCQTKWG 116
 Db 135 eywdqld-hllncyqktrcsf-kygoekl-rmsikmgfllvtcdcfkrdldkkel 191
 Qy 117 tlkEYESCHEGICPFllTECPACGGLVRLSEKHHTQDECPKRKSLSCQHC-RAPCSHDL 175
 Db 192 ethykctqmpvldesqgsvk-ierkeidhndcentidpckyfeagckveamrse-l 249
 Qy 176 EVHAYECPFEPllTC-DCCSKKRIPRETFOPHY-RACSCGVLCRFHVTGCS-EMVETNL 232
 Db 250 qmh-lervhmqymglliek-ltngvqgsktch-d-ellkkiedslvlkfcd-ac-lk 303

RA LOVERING R., HANSON I.M., BORDEN K.L.B., MARTIN S., O'REILLY N.J.,
RA EVAN G.I., HAMMAN D., PAPPIN D.J.C., TROWSDALE J., FREEMONT P.S.;
RL PROG. NATL. ACAD. SCI. U.S.A. 90:2112-2116(1993).
CC -I- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -I- SIMILARITY: CONTAINS A CHC4-CLASS ZINC FINGER.
DR EMBL; Z14000; Z14000.
DR PIR; A47380; A47380.
DR HSSP; P28990; 1CHC.
DR PROSITE; PS00518; ZINC_FINGER_CHC4.
KM ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.
FT ZN FING 19 58 CHC4-TYPE.
FT DOMAIN 176 231 GLY-RICH.
FT DOMAIN 285 348 GLY-RICH.
FT DOMAIN 112 175 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 377 AA; 39145 MW; 716288 CN;

Query Match 3.8%; Score 141; DB 7; Length 377;
Best Local Similarity 32.6%; Pred. No. 1,69e-06;
Matches 15; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

Db 13 l3aelmpcldlmlkmttkhechrfcscdrtlrgnkspte 58
Qy 28 LEARYTCSAGKNILRRPQA-OCGRYCSCLTSLSSGRQNCAC 72

RESULT 9
ID COP1 ARATH STANDARD; PRT; 675 AA.
AC P43254;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1).
GN COP1 OR FUS1.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOT; PLANTA; EMNORPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPRALES; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=WHOLE SEEDLING;
RX MEDLINE; 93046683.
RA DENG X.-W., MATSUI M., WEI N., WAGNER D., CHU A.M., FELDMANN K.A.,
RA QUILP P.H.;
RL CELL 71:791-801(1992).
CC -I- FUNCTION: ACTS AS A REPRESSOR OF PHOTOMORPHOGENESIS IN DARKNESS,
CC AND LIGHT STIMULI ABROGATE THIS SUPPRESSIVE ACTION. COULD FUNCTION
CC AS A NEGATIVE TRANSCRIPTIONAL REGULATOR CAPABLE OF DIRECT
CC INTERACTION WITH COMPONENTS OF THE G PROTEIN SIGNALING PATHWAY.
CC -I- SUBCELLULAR LOCATION: NUCLEAR.
CC -I- SIMILARITY: CONTAINS A CHC4-CLASS ZINC FINGER.
CC -I- SIMILARITY: BELONGS TO THE BETA TRANSDUCIN FAMILY; CONTAINS
CC TRP-ASP DOMAINS.
DR EMBL; L24437; L24437.
DR PROSITE; PS00518; ZINC_FINGER_CHC4.
DR PROSITE; PS00678; G BETA_REPEATS.
KM ZINC-FINGER; NUCLEAR PROTEIN; REPEAT.
FT ZN FING 52 89 CHC4-TYPE.
SQ SEQUENCE 675 AA; 76260 MW; 2370819 CN;

Query Match 3.6%; Score 135; DB 2; Length 675;
Best Local Similarity 31.1%; Pred. No. 1,40e-05;
Matches 14; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

46 ldkdllepcmqkikltaacsfycfcmkthlrnks-dcpcc 89

Qy 28 LEAKYLSACNKLIRRFQACGHRVCSFLTSLSSGPNCAAC 72

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RESULT 10
ID 2G48 XENIA STANDARD; PRT; 647 AA.
AC P18723;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE GASTRULA ZINC FINGER PROTEIN XLOC48.2 (FRAGMENT).
OS XENOPUS LAEVIS (AFRICAN CLAMPED FROG).
OC EUARHOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE OF 1-339 FROM N.A.
RX MEDLINE; 89345612.
RA KNOCHEL W., PÖTING A., KOSTER M., EL BARADI T., NIETZELD W.,
RA BOWMEESTER T., PIELER T.;
RA PROC. NATL. ACAD. SCI. U.S.A. 86:6097-6100 (1989).
RN [2]
RP SEQUENCE OF 312-647 FROM N.A.
RX MEDLINE; 90040698.
RA NIETZELD W., EL-BARADI T., MENTZEL H., PIELER T., KOESTER M.,
RA PÖTING A., KNOCHEL W.;
RL J. MOL. BIOL. 208:639-659 (1999).
DR EMBL; M25871; M25871.
DR PIR; F33282; F33282.
DR PIR; S06573; S06573.
DR HSSP; P07248; IARD.
DR PROSITE; P500028; ZINC FINGER C2H2.
KM ZINC-FINGER; METAL-BINDING; DNA-BINDING; REPEAT.
FT ZN_FING 317 339 C2H2-TYPE.
FT ZN_FING 345 367 C2H2-TYPE.
FT ZN_FING 373 395 C2H2-TYPE.
FT ZN_FING 401 423 C2H2-TYPE.
FT ZN_FING 429 451 C2H2-TYPE.
FT ZN_FING 457 479 C2H2-TYPE.
FT ZN_FING 485 507 C2H2-TYPE.
FT ZN_FING 513 535 C2H2-TYPE.
FT ZN_FING 540 563 C2H2-TYPE.
FT ZN_FING 541 563 C2H2-TYPE.
FT ZN_FING 569 591 C2H2-TYPE.
FT ZN_FING 597 619 C2H2-TYPE.
FT ZN_FING 625 647 C2H2-TYPE.
FT NON_TER 647 647
SQ SEQUENCE 647 AA; 73054 MM; 2104456 CN;
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Query Match 3.4%; Score 126; DB 9; Length 647;
Best Local Similarity 28.4%; Pred. No. 3.04e-04;
Matches 33; Conservative 20; Mismatches 57; Indels 6; Gaps 6;

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Db 365 rnhlgekfscseceqckfwtalllhhthtgdskfcdacqckfkkfslrhtkht 424
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 97 RREVESLAVCPNDG-C-TKGTGLKEYESCHGICPLLTETCPAC-KGLVRLSP-KSHHT 152
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
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Db 425 gee-pfvcsecegfafapqldlhmrlhtge-t-fscsdqckctfgradlnvrrt 478
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Qy 133 EQGCPKRSLSQHCGRAPCSHVDLHVHYCKRPFLTCDGCGKKRIPRETFQDHVRA 208

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RESULT 11
ID YNNI CAEEL STANDARD; PRT; 160 AA.
AC 003605;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
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DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 18.7 KD PROTEIN T02C1.1 IN CHROMOSOME III.

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GN T02C1.1.
OS CAENORHABDITIS ELEGANS.
OC EUARHOTA; METAZOA; ACCELLOMATES; NEMATODA; SECCERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RC MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DUBBIN B., FAVELLO A., FRASER A.,
RA FULTON L., GARDNER A., GREEN P., HAKINS T., HILLIER L., JIER M.,
RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
RA LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIRKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,
RA SIMS M., SWALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
RA SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
RA WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
RA WOHLDMAN P.;
RL NATURE 368:32-38 (1994).
CC -1- SURCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- SIMILARITY: CONTAINS A C3H04-CLASS ZINC FINGER.
DR EMBL; Z19156; Z19156.
DR PIR; S28290; S28290.
DR WORMREP; T02C1.1; CE00312.
DR PROSITE; P500518; ZINC FINGER C3HC4.
KM HYPOTHETICAL PROTEIN; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.
FT ZN_FING 8 45 C3HC4-TYPE.
SQ SEQUENCE 160 AA; 18675 MM; 132007 CN;
```

Query Match 3.2%; Score 120; DB 9; Length 160;
Best Local Similarity 31.8%; Pred. No. 2.21e-03;
Matches 14; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

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Db 3 dedfccavcdiffvepcilceghaycfcieshlnl-n-ekpck 45
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy 29 EAKYLSACNKLIRRFQACGHRVCSFLTSLSSGPNCAAC 72
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RESULT 12
ID TPMS HUMAN STANDARD; PRT; 227 AA.
AC P10465;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE (FRAGMENT).
GN TPML OR TMSA.
OS HOMO SAPIENS (HUMAN).
OC EUARHOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER;
RC MEDLINE; 88333013.
RA COLOTE S., WIDADA J.S., FERRAZ C., BONHOMME F., MARTI J.,
RA LIAUTAUD J.-P.;
RL J. MOL. EVOL. 27:228-235 (1988).
CC -1- FUNCTION: THE FUNCTION OF TROPOMYOSIN IN SMOOTH MUSCLE AND NON-
CC MUSCLE CELLS IS NOT CLEAR.
CC -1- SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE
CC EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.
CC -1- ALTERNATIVE PRODUCTS: THE VARIOUS TROPOMYOSIN ISOFORMS ARE
```

CC PRODUCED BY ALTERNATIVE MRNA SPLICING.

DR EMBL, X12369; X12369.

DR PIR, S05585; S05585.

DR MIM, 191010; 11TH EDITION.

DR PROSITE, P500326; TROPOMYOSIN.

KM MUSCLE PROTEIN; COILED COIL; REPEAT; ALTERNATIVE SPLICING.

FT NON TER 1 1

SQ SEQUENCE 227 AA; 26576 MW; 225728 CN;

Query Match

Best Local Similarity 19.2%; Pred. No. 3.06e-03;

Matches 15; Conservative 30; Mismatches 31; Indels 2; Gaps 2;

Db 124 etaeleegvqleeqrlmidslesinaedkysqgedtyee-llvleklkkaetra 182

Qy 270 QRCQLLEQKIAFTFIVICVLRNREVERAVATALACS-RQHRLDQKITALSNVQLERST 328

Db 183 efaervtkleksiidle 200

Qy 329 GKRLAMADLEQKXSELE 346

RESULT 13

ID BRCL HUMAN STANDARD; PRT; 1863 AA.

AC P38398;

DT 01-OCT-1994 (REL. 30, CREATED)

DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)

DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)

DE BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN.

GN BRCL.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

NM (1)

RP SEQUENCE FROM N.A., AND VARIANT ARG-1775.

RX MEDLINE; 95025896.

RA MIKI Y., SWENSEN J., SHATTUCK-EIDENS D., FUTREAL P.A., HARSHMAN K.,

RA TAVTIGIAN S., LIU Q., COCHRAN C., BENNETT L.M., DING W., BELL R.,

RA ROSENTHAL J., HUSEY C., TRAN T., MCCLURE M., FRYE C., HATTER T.,

RA PHELPS R., HAUGEN-STRANO A., KATCHER H., YAKIMO K., GHOLAMI Z.,

RA SHAFFER D., STONE S., BAYER S., WRAY C., BOGDEN R., DAYANATH P.,

RA WARD J., TONIN P., NAROD S., BRISTOW P.K., NORRIS F.H., HEVERING L.,

RA MORRISON P., ROSTECK P., LAI M., BARRETT J.C., LEMIS C., NEUHUSEN S.,

RA CANNON-ALBERTIGHT L., GODIGAN D., WISEMAN R., KAMB A., SKOLNICK M.H.,

RL SCIENCE 266:66-71(1994).

RN (12)

RP VARIANTS LEU-1637, GLU-1708 AND ARG-1775.

RX MEDLINE; 95025878.

RA FUTREAL P.A., LIU Q., SHATTUCK-EIDENS D., COCHRAN C., HARSHMAN K.,

RA TAVTIGIAN S., BENNETT L.M., HAUGEN-STRANO A., SWENSEN J., MIKI Y.,

RA EDDINGTON K., MCCLURE M., FRYE C., WEAVER-FELHAUS J., DING W.,

RA GHOLAMI Z., SOEDERKVIIST P., TERRY L., JHANVAR S., BERCHUK A.,

RA IGLEHART J.D., MARKS J., BALLINGER D.G., BARRETT J.C., SKOLNICK M.H.,

RA KAMB A., WISEMAN R.,

RL SCIENCE 266:120-122(1994).

RN (13)

RP VARIANTS BC GLY-64 AND GLY-1443, AND VARIANTS ALA-772 AND ASN-1040.

RA CASTILLA L.H., COUCH F.J., ERDOS M.R., HOSKINS K.F., CALZONE K.,

RA GABER J.E., BOYD J., LOBIN M.B., DESHANO M.L., BRODY L.C.,

RA COLLINS F.S., WEBER B.L.,

RL NAT. GENET. 8:387-391(1994).

RN (4)

RP VARIANTS BC G-61, AND VARIANTS R-356, G-1038, N-1040; R-1183 & G-1613.

RA FRIEDMAN L.S., OSTERMEYER E.A., SZABO C.I., DOWD P., LYNCH E.D.,

RA ROWELL S.E., KING M.-C.,

RL NAT. GENET. 8:399-404(1994).

CC -1- FUNCTION: NOT KNOWN, MAY REGULATE GENE EXPRESSION.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

CC -1- DISEASE: BREAST CANCER (BC) IS AN EXTREMELY COMMON MALIGNANCY,

CC AFFECTING ONE IN EIGHT WOMEN DURING THEIR LIFETIME. A POSITIVE

CC FAMILY HISTORY HAS BEEN IDENTIFIED AS MAJOR CONTRIBUTOR TO RISK OF

CC DEVELOPMENT OF THE DISEASE, AND THIS LINK IS STRIKING FOR EARLY-

CC ONSET BREAST CANCER. MUTATIONS IN BRCA1 ARE THOUGHT TO BE

CC RESPONSIBLE FOR 45% OF INHERITED BREAST CANCER AND MORE THAN 80%

CC OF INHERITED BREAST AND OVARIAN CANCER (BOC).

CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL, U14680; U14680.

DR MIM, 113705; 11TH EDITION.

DR PROSITE, P500518; ZINC FINGER C3HC4.

KM ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN; DISEASE MUTATION;

KM POLYMORPHISM; ANTI-ONCOGENE.

FT 2N FING 24 64 C3HC4-TYPE.

FT VARIANT 61 61 C -> G (IN BREAST CANCER).

FT VARIANT 64 64 C -> G (IN BREAST CANCER).

FT VARIANT 356 356 Q -> R.

FT VARIANT 772 772 V -> A.

FT VARIANT 1038 1038 E -> G.

FT VARIANT 1040 1040 S -> N.

FT VARIANT 1183 1183 K -> R.

FT VARIANT 1443 1443 R -> G (IN BREAST CANCER).

FT VARIANT 1613 1613 S -> G.

FT VARIANT 1637 1637 P -> L (IN OVARIAN CANCER).

FT VARIANT 1708 1708 A -> E (IN BREAST CANCER).

FT VARIANT 1775 1775 M -> R (IN BREAST CANCER).

SQ SEQUENCE 1863 AA; 207720 MW; 16213725 CN;

Query Match 3.2%; Score 120; DB 1; Length 1863;
Best Local Similarity 33.3%; Pred. No. 2.21e-03;

Matches 15; Conservative 11; Mismatches 16; Indels 3; Gaps 2;

Db 20 kilepcleleikepvckcdhlfckmlklmqkqpsqpic 64

Qy 31 KYL-CSACGNILRRPQACGCHRYCSFCITSIIS--SGPQNCAC 72

RESULT 14

ID OMPA THEMA STANDARD; PRT; 400 AA.

AC Q01969;

DT 01-JUL-1993 (REL. 26, CREATED)

DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)

DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)

DE OUTER MEMBRANE PROTEIN ALPHA PRECURSOR.

GN OMP-ALPHA.

OS THERMOTOGA MARITIMA.

OC PROKARYOTA; NOT YET CLASSIFIED.

RN (11)

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=MSB8 / DSM 3109;

RX MEDLINE; 93049187.

RA ENGEL A.M., CEJKA Z., LUPAS A., LOTTSPREICH F., BAUMEISTER W.,

RL EMBO J. 11:4369-4378(1992).

CC -1- FUNCTION: LINKS THE OUTER MEMBRANE TO THE INNER MEMBRANE. LONG

CC FIBROUS PROTEIN THAT COULD SERVE TO SEPARATE THE TWO MEMBRANES.

CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.

CC -1- SIMILARITY: CONTAINS A COPY OF THE S-LAYER HOMOLOGY (SLH) DOMAIN.

DR EMBL, X68276; X68276.

DR PIR, S28022; S28022.

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(TM)

MPsrch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Dec 10 07:08:41 1996; MasPar time 10.68 Seconds
446.743 Million cell updates/sec
Tabular output not generated.

Title: >US-08-446-915-4
Description: (1-501) from US08446915.pep
Perfect Score: 3702
Sequence: 1 MAAASVTSPGSELLQPGFS.....NSYVDALIFKAIWDLTGL 501

Scoring table: PAM 150
Gap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq24
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 35.625; Variance 156.291; scale 0.228

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	3700	99.9	501 15	R90578				Mouse TRAF2.	0.00e+00
2	972	26.3	409 15	R90577				Mouse TRAF1.	3.96e-19
3	131	3.5	41 16	R91212				RIN1 zinc finger doma	5.64e-02
4	120	3.2	1863 16	R91208				BRCA1, breast and ova	3.81e-01
5	120	3.2	1863 15	R16641				BRCA1 protein.	3.81e-01
6	111	3.0	41 16	R91210				BRCA1 polypeptide zin	1.74e+00
7	99	2.7	252 1	P94369				Fusion protein cong.	1.24e+01
8	101	2.7	700 15	R89145				Chondroitinase AC.	9.00e+00
9	96	2.6	45 16	R91211				RP1 zinc finger doma	2.00e+01
10	95	2.6	200 10	R53430				Human/rat chimeric ci	2.34e+01
11	95	2.6	200 10	R53428				Human/rat chimeric ci	2.34e+01
12	95	2.6	200 10	R53429				Human/rat chimeric ci	2.34e+01

13	96	2.6	365 1	P91461	Rpt-1 clone cDNA inse	2.00e+01
14	98	2.6	475 3	R15148	Ro/SSA autoantigen.	1.46e+01
15	97	2.6	576 12	R66929	AMML chromosome inv(1	1.71e+01
16	97	2.6	816 12	R66931	AMML chromosome inv(1	1.71e+01
17	97	2.6	885 12	R66930	AMML chromosome inv(1	1.71e+01
18	96	2.6	1093 8	R42818	TNF.	2.00e+01
19	97	2.6	2482 14	R72826	Human mitotin.	1.71e+01
20	92	2.5	263 1	R03348	VP2 sequence for HRV	3.74e+01
21	92	2.5	462 1	R05766	Portion of peptide an	3.74e+01
22	94	2.5	594 6	R34936	CENP-B.	2.74e+01
23	94	2.5	854 12	R66052	Human NMDA receptor s	2.74e+01
24	94	2.5	908 12	R66053	Human NMDA receptor s	2.74e+01
25	94	2.5	1427 2	R10534	Human 160kD mediator	4.37e+01
26	91	2.5	3084 2	P94758	Sequence of mouse lam	2.74e+01
27	94	2.5	161 7	R37707	N-terminal delta14/C-	6.92e+01
28	88	2.4	187 7	R37705	Delta14 hCNTF.	6.92e+01
29	88	2.4	192 6	R32856	Sequence of neurotrop	6.92e+01
30	88	2.4	200 10	R53432	Human/rat chimeric ci	6.92e+01
31	89	2.4	200 1	R06234	Human sciatic nerve c	5.94e+01
32	88	2.4	200 6	R31950	Sequence of human cil	6.92e+01
33	88	2.4	200 10	R53424	Human/rat chimeric ci	6.92e+01
34	88	2.4	200 11	R58303	Human ciliary neutrop	6.92e+01
35	88	2.4	200 3	R13960	Human CNTF.	6.92e+01
36	88	2.4	200 7	R34431	Sequence of human cil	6.92e+01
37	88	2.4	200 10	R53432	Human/rat chimeric ci	6.92e+01
38	88	2.4	200 7	R37819	Sequence of human cil	6.92e+01
39	88	2.4	200 13	R70146	Human CNTF.	6.92e+01
40	88	2.4	200 10	R53425	Human/rat chimeric ci	6.92e+01
41	88	2.4	200 14	R83966	Ciliary neurotrophic	6.92e+01
42	88	2.4	673 1	R06552	Human 5-lipoxygenase	6.92e+01
43	89	2.4	775 3	P50121	Sequence of a polypep	5.94e+01
44	88	2.4	775 2	P70417	Polypeptide with IgE	6.92e+01
45	90	2.4	3685 1	P90290	Human Duchenne muscl	5.10e+01

ALIGNMENTS

RESULT	1
ID	R90578 standard; Protein; 501 AA.
AC	R90578;
DT	09-APR-1996 (first entry)
DE	Mouse TRAF2.
KW	TRAF2; tumour necrosis factor receptor associated factor 2;
KM	TNF; CD40.
OS	Mus musculus.
FH	Key
FT	Domain
FT	/label= TRAF_domain
FT	/label= 275..351
FT	/label= leucine_zipper_region
PN	W09533051-A1.
PD	07-DEC-1995.
PF	25-MAY-1995; U06639.
PR	27-MAY-1994; US-250858.
PR	28-OCT-1994; US-331394.
PR	22-MAY-1995; US-446915.
PA	(GETH) GENENTECH INC.
PI	Goeddel DV., Rothe M.
DR	NTF; 96-0493310/05.
DR	N-PSDB; T12262.
PT	Tumour necrosis factor (TNF) receptor-associated factors - Involved
PT	in mediation of biological activities of TNF and CD40 ligands
PS	Claim 8; Page 75-76; 116pp; English.
CC	Mouse tumour necrosis factor receptor associated factor 2 (TRAF2)

CC (R80S0518) is a new factor capable of specific association with the
CC intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40,
CC and is involved in the mediation of TNF and CD40 ligand biological
CC activities. Recombinant TRAF2 is obtd. by expression in host cells
CC of a cDNA clone (112262) isolated using a yeast two-hybrid assay.
CC It is used to identify inhibitors of activities of TNF-R2, CD40
CC and/or LMP1 oncogene, e.g. for treatment of endotoxic (septic)
CC shock and rheumatoid arthritis.
SQ Sequence 501 AA;

Query Match	99.9%;	Score 3700;	DB 15;	Length 501;
Best Local Similarity	99.8%;	Pred. No. 0.00e+00;		
Matches 500; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

D	b	1	maasvtrpsgsllelpgfsxhtllgttlaakyljseacknllrrpfbaqgchryscfclte	60
Q	y	1	MAASVTRPSGSLLELPGFSGKTLGTRLEAKYLCACKNLTIRPFOACGGRYCSCLTS	60
D	b	61	ilssgpdcaacyeqglveegisillessafduaarveeslpavcndctwyltke	120
Q	y	61	ILSSGPDCAACYEGIVEEGISITLESSAFDUAARVEESLPVPCNDCTWYLTKE	120
D	b	121	yeecheqjclfilltecpackglvrlsekehhegecpkrlsecqctrapeshvdlvhye	180
Q	y	121	YEECHGEQJCLLLTECPACKGLVRLSEKEHHGECPKRLSQCHRAPCSHVDLEVHYE	180
D	b	181	vcpkfpltcddcgckkkipretfgdhvascercvtorfhtvgsesametenlqdelgrl	240
Q	y	181	VCPKFP LTCDDCGCKKIIPRETFGDHVASCERCVTORFHTVGSSEMETENLDHDLRL	240
D	b	241	rehllallseflseagspptlnqgpyllqrcqlleqkistfenvvclhrerevratrta	300
Q	y	241	REHLLALLSEFLSEAGSPPTLNQGPYLLQRCQLLEQKISTFENVVCLHREVERAVTAR	300
D	b	301	eeacgrhltdckdkealsnkvqleziqglkelamadlegkveselvsevdgyflwklsid	360
Q	y	301	EACSRQHRLDDCKDEALSNKVQLERISIGKLAMADLEGKVESELEVSTVDGYFLKLSID	360
D	b	361	ftrkrgaeavagtrpaifspafyeryykmclrvlyngdqtgrgfhslsffvmykpnnda	420
Q	y	361	FTKRQGEAVAGRPAIFSPAFYERYYKMCRLRVLYNGDQTRGFHLSLFFVMYKPNDA	420
D	b	421	llswpfnqkvvtlmlldhnmrehvldaftrpvtseasfqrpvsdnniaasgcplfcvpykmea	480
Q	y	421	LLOMPFNQKVTLMLDHNHREHVLDAFRPVTSSFRPVSDDNIIASGCLFCVPYSKMEA	480
D	b	481	knayvrdaifikaivdlcgl	501
Q	y	481	KNSYVRDAIFIKAIYDLTGL	501

FT	Region	/label= leucine zipper region
FT	Domain	180..409
FT	/label= TRAF_domain	
FT	Region	183..259
FT	/label= leucine zipper region	

PN M09533051-A1.
PD 07-DEC-1995.
PE 25-MAY-1995; U06639.
PR 27-MAY-1994; US-250858.
PR 28-OCT-1994; US-331394.
PR 22-MAY-1995; US-446915.
PA (GENTH) GENENTECH INC.
PI Goeddel DV, Rothe M;
DR WPl; 96-049310/05.
DR N-PSDB; 171261.
PT Tumour necrosis factor (TNF) receptor-associated factors - involved
PT in mediation of biological activities of TNF and CD40 ligands
PS Claim 8; Page 71-72; 11pp; English.
PS Mouse tumour necrosis factor receptor associated factor 1 (TRAF1)
CC (R90557) is a new factor capable of specific association with the
CC intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40,
CC and is involved in the mediation of TNF and CD40 ligand biological
CC activities. Recombinant TRAF1 is obt'd. by expression in host cells
CC of a cDNA clone (T112261) isolated from murine interleukin-2-dependent
CC cytotoxic T-cell line CT6. It is used to identify inhibitors of
CC activities of TNF-R2, CD40 and/or LMP1 oncogene, e.g. for treatment
CC of endotoxic (septic) shock and rheumatoid arthritis.
SQ Sequence 409 Aa;

Query Match 26.3%; Score 912; DB 15; Length 409;
Best Local Similarity 54.0%; Pred. No. 3.96-79;
Matches 121; Conservative 61; Mismatches 41; Indels 1; Gaps 1

[illegible]

RESULT	3
ID	R91212 standard; Peptide: 41 AA.
AC	R91212;
DT	05-JUN-1996 (first entry)
DE	RIM1 zinc finger domain.
KM	RIM1; BRCA1; breast cancer; ovary cancer; predisposing gene;
KM	susceptibility gene; protein replacement therapy; diagnosis
KM	prognosis.
OS	Not specified.
PN	W09605307-A2.
PD	22-FEB-1996.
PF	11-AUG-1995; U10703.
PR	12-AUG-1994; US-2899221.
PR	02-SEP-1994; US-300266.
PR	16-SEP-1994; US-308104.
PR	29-NOV-1994; US-348824.
PR	24-MAR-1995; US-409305.
PR	07-JUN-1995; US-488011.
PR	07-JUN-1995; US-483554.

Query Match	2.7%	Score 99	DB 1	Length 252
Best Local Similarity	23.2%	Pred. No. 1.24e+01		
Matches	29	Conservative	35	Mismatches 55; Indels 6; Gaps 5
Sequence	252 AA			
Db	102	vdvdedraeaelekkreaqallheteskaeevarklamreadleraeaeegenkivel	161	
Qy	227	VERENKQHEIQ-RLEHIALALLSFTLEQASPEPTINQVGPGL--IQ-RCQILRQKIAIF	282	
Db	162	eeeltrvgmnlkselvwsekalqedsye--eqititsarlkneatraefaeasvnhkqke	220	
Qy	283	ENTVCAVLAIREVERAVATAE-ACSRQRHLDQDKIEALSNKVOEDERSIGIKDLAMADLEOK	341	
Db	221	vdle 225		
Qy	342	VSELE 346		
RESULT	8			
ID	R89145	standard; Protein; 700 AA.		
AC	R89145			
DT	22-APR-1996	(first entry)		
DE	Chondroitinase AC.			
KM	Chondroitinase AC; chondroitinase B; chondroitin lyase;			
OS	chondroitin sulphate.			
FT	Flavobacterium heparinum.			
FT	Key	location/Qualifiers		
FT	Peptide	1..23		
FT	/label= Sig_peptide			
FT	Protein	24..700		
PN	/label= Mat_protein			
PD	W09601894-A1.			
PE	25-JAN-1996.			
PR	07-JUL-1995; U08560.			
PR	08-JUL-1994; U5-272247.			
PA	(IBEX-) IBEX TECHNOLOGIES R & D INC.			
P1	Bennett DC, Fink D, Gu K, Laliberte M, Linhardt R;			
P1	Tkalec AL, Zimmermann J;			
DR	WPI; 96-097624/10.			
DR	N-PSDB; T10316.			
PT	Purification of chondroitinase AC and chondroitinase B - using			
PT	osmotic shock and successive chromatography to fractionate the			
PT	proteins			
PS	Claim 7; Page 30-33; 53pp; English.			
CC	Flavobacterium heparinum chondroitinase AC (R89145) and			
CC	chondroitinase B (R89146) are capable of degrading chondroitin			
CC	sulphate polysaccharides. The enzymes, which have catalyzed			
CC	mol.wts. of 77,169 and 53,563, respectively, can be obt. by			
CC	purification from F. heparinum cells or by expression of the			
CC	encoding genes (see T10316 and T10317) in host cells. They are			
CC	useful as tools in determining the role of chondroitin sulphates			
CC	in modulating cellular events, and can also be used to develop			
CC	therapeutic reagents.			
Qy	Sequence	700 AA;		
Query Match	2.7%	Score 101	DB 15	Length 700
Best Local Similarity	31.9%	Pred. No. 9.00e+00		
Matches	22	Conservative	17	Mismatches 23; Indels 7; Gaps 5

Query Match	2.7%	Score 99	DB 1	Length 252
Best Local Similarity	23.2%	Pred. No. 1.24e+01		
Matches	29	Conservative	35	Mismatches 55; Indels 6; Gaps 5
Sequence	252 AA			
Db	102	vdvdedraeaelekkreaqallheteskaeevarklamreadleraeaeegenkivel	161	
Qy	227	VERENKQHEIQ-RLEHIALALLSFTLEQASPEPTINQVGPGL--IQ-RCQILRQKIAIF	282	
Db	162	eeeltrvgmnlkselvwsekalqedsye--eqititsarlkneatraefaeasvnhkqke	220	
Qy	283	ENTVCAVLAIREVERAVATAE-ACSRQRHLDQDKIEALSNKVOEDERSIGIKDLAMADLEOK	341	
Db	221	vdle 225		
Qy	342	VSELE 346		
RESULT	8			
ID	R89145	standard; Protein; 700 AA.		
AC	R89145			
DT	22-APR-1996	(first entry)		
DE	Chondroitinase AC.			
KM	Chondroitinase AC; chondroitinase B; chondroitin lyase;			
OS	chondroitin sulphate.			
FT	Flavobacterium heparinum.			
FT	Key	location/Qualifiers		
FT	Peptide	1..23		
FT	/label= Sig_peptide			
FT	Protein	24..700		
PN	/label= Mat_protein			
PD	W09601894-A1.			
PE	25-JAN-1996.			
PR	07-JUL-1995; U08560.			
PR	08-JUL-1994; U5-272247.			
PA	(IBEX-) IBEX TECHNOLOGIES R & D INC.			
P1	Bennett DC, Fink D, Gu K, Laliberte M, Linhardt R;			
P1	Tkalec AL, Zimmermann J;			
DR	WPI; 96-097624/10.			
DR	N-PSDB; T10316.			
PT	Purification of chondroitinase AC and chondroitinase B - using			
PT	osmotic shock and successive chromatography to fractionate the			
PT	proteins			
PS	Claim 7; Page 30-33; 53pp; English.			
CC	Flavobacterium heparinum chondroitinase AC (R89145) and			
CC	chondroitinase B (R89146) are capable of degrading chondroitin			
CC	sulphate polysaccharides. The enzymes, which have catalyzed			
CC	mol.wts. of 77,169 and 53,563, respectively, can be obt. by			
CC	purification from F. heparinum cells or by expression of the			
CC	encoding genes (see T10316 and T10317) in host cells. They are			
CC	useful as tools in determining the role of chondroitin sulphates			
CC	in modulating cellular events, and can also be used to develop			
CC	therapeutic reagents.			
Qy	Sequence	700 AA;		
Query Match	2.7%	Score 101	DB 15	Length 700
Best Local Similarity	31.9%	Pred. No. 9.00e+00		
Matches	22	Conservative	17	Mismatches 23; Indels 7; Gaps 5

[illegible]

RESULT 9

ID	R91211	standard; Peptide; 45 AA.
AC	R91211;	
PT	05-JUN-1996	(first entry)
DE	RP1; zinc finger domain.	
DE	RP1; BRCAL; breast cancer; ovary cancer; predisposing gene;	
KW	susceptibility gene; protein replacement therapy; diagnosis;	
OS	prognosis.	
OS	Mus sp.	
PN	M09605307-82.	
PD	22-FEB-1996.	
PF	11-AUG-1995; U10203.	
PR	12-AUG-1994; US-289221.	
PR	02-SEP-1994; US-300266.	
PR	16-SEP-1994; US-308104.	
PR	29-NOV-1994; US-348824.	
PR	24-MAR-1995; US-409305.	
PR	07-JUN-1995; US-488011.	
PR	07-JUN-1995; US-483554.	
PR	07-JUN-1995; US-487002.	
PA	(MYRI-) MYRIAD GENETICS INC.	
PA	(UTAH) UNIV UTAH RES FOUND.	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PA	Futreal AP, Goldgar DE, Hershman KD, Kamb A, Miki Y;	
PI	Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;	
PI	Miseman RW;	
PT	WPI; 96-139703/14.	
PT	New isolated human cancer predisposing gene, BRCAL - used to develop	
PT	prods. for diagnosis, prognosis and therapy of cancers, partic.	
PT	breast and ovarian cancers	
PS	Example 8; Page 172; 190pp; English.	
CC	A sequence (R91210) near the amino terminus of the human BRCAL	
CC	polypeptide (R91208) shows considerable homology to zinc finger	
CC	domains, including RPT1 (R91211) a protein that appears to be a	
CC	negative regulator of the interleukin-2 receptor in mouse, RNL1	
CC	(R91212) a DNA-binding protein that includes a RING-finger motif	
CC	related to the zinc finger, and RPT1 (R91213) a putative	
CC	transcription factor that is the N-terminal domain of the RET	
CC	oncogene product.	
CC	Sequence 45 AA;	
CC	Sequence 45 AA;	
DB	1	cpic1ellkpevdschfcract 26
DB	1:	1::1:1 1:1 1:1 1:1
QY	34	CSACKN1LRPFQAGCHRYCSFCLT 59
RESULT	10	
ID	R53430	standard; protein; 200 AA.
AC	R53430;	
PT	13-DEC-1994	(first entry)

DE	Human/rat chimeric ciliary neurotrophic factor RPN222.
KM	Human ciliary neurotrophic factor; hCNTF; mutant; variant;
KM	receptor binding; enhance; nervous system disorder; treatment;
KM	chimeric protein; electrophoretic mobility.
OS	Chimeric Homo sapiens.
OS	Chimeric Rattus sp.
FM	Key Location/Qualifiers
FT	Misc_difference 53
FT	/note="Ala is subst. by Val"
FT	Misc_difference 67
FT	/note="Ileu is subst. by Met"
PN	W09409134-A.
PD	28-Apr-1994.
PF	08-Oct-1993; U09649.
PR	09-Oct-1992; US-959284.
PI	(REG-) REGENERON PHARM INC.
PA	Panayotatos N;
DR	WPI; 94-151319/18.
PT	Modified human ciliary neurotrophic factor - having a glutamine
PT	63 to arginine substn to enhance receptor binding and increase
PT	biological activity.
PS	Example 1; Page 32; 46pp; English.
PS	Recombinant human and rat CNTF have the same number of amino acids and
CC	similar mass (22.7 KD). On reducing SDS-PAGE gels, however, recombinant
CC	hCNTF migrates as a protein of mol.wt. 27.5 KD while rat CNTF
CC	migrates as expected. The hCNTF also has 4 times lower biological
CC	activity towards chick ciliary ganglion neurons than rat CNTF. The
CC	rat CNTF competes for binding to the human or rat receptor better
CC	than human CNTF. A series of chimeric proteins was prepared in
CC	which part of the human CNTF was replaced by the corresp. rat
CC	sequence (see R53423-R53432). It was found that all variants with
CC	an arginine residue at position 63 display the mobility of rat
CC	CNTF. Human CNTF in which Gln at position 63 is replaced by Arg is
CC	claimed.
CC	Sequence 200 Aa;
CC	Sequence

Query Match	2.6%;	Score 95;	DB 10;	length 200;
Best Local Similarity	35.6%;	Pred. No. 2.34e+01;		

Matches	21; Conservative	13; Mismatches	21; Indels	4; Gaps
D6	65	seenteaerlqen-lqayrt-fhvl-arlledqgwhfpte-g-dfhqahntlllqraaf	119	
Oy	224	SMETEDNADHETQRIAREHMLALISTLEAQASGCTANQVGEELAQICQULETKATAT	282	

RESULT 11

ID	R53428 standard; protein; 200 AA.
AC	R53428;
DT	13-DEC-1994 (first entry)
DE	Human/rat chimeric ciliary neurotrophic factor RBN218.
KE	Human ciliary neurotrophic factor; hCNTF; mutant; variant;
KW	receptor binding; enhance; nervous system disorder; treatment;
OS	chimeric protein; electrophoretic mobility.
OS	Chimeric Homo sapiens.
OS	Chimeric Rattus sp.
PH	Key
PH	Location/Qualifiers
FT	Misc difference 35
FT	/note= "Pthr is subst. by Met"
FT	Misc difference 53
FT	/note= "Ala is subst. by Val"
FT	Misc difference 56
FT	/note= "Met is subst. by Val"
FT	Misc difference 63
FT	/note= "Gln is subst. by Arg"

Dec 10 06:53

US-08-446-915-4.rtf

15

AC R15148; DT 14-FEB-1992 (first entry)
DE Ro/SSA autoantigen.
KW Autoantibody; autoantigen; SLE; systemic lupus erythematosus.
PN Homo sapiens.
MO W091171-A.
PD 14-NOV-1991.
PE 07-MAY-1991; U03139.
PR 07-MAY-1990; US-520270.
PA (OKLA-) OKLAHOMA MED RES FO.
PI Frank MB, Itoh K;
DR WPI; 91-353712/48.
DR N-PSDB; Q14798.
PT DNA encoding an Ro-SSA autoantigen - useful for diagnosing
PT auto-immune disorders or presence of auto-antibodies
PS Disclosure; Fig 2; 41pp; English.
CC A cDNA library (from human thymus mRNA) in lambda gtl1 was screened
CC with serum from a patient having systemic lupus erythematosus. Two
CC clones were reactive with sera (from a panel of lupus patients)
CC which cont'd. autoantibodies against 52 kD protein.
CC Both the cDNA and the protein expressed from it, or portions of it,
CC are useful as diagnostic agents in the identification of patients
CC having autoantibodies and in the identification and analysis of
CC the structural and functional properties of the autoantigen and for
CC application in immunotherapeutic regimens.
SQ Sequence 475 AA;

	Query Match	2.6%	Score 98;	DB 3;	length 475;
	Best Local Similarity	28.2%;	Pred. No.	1,46e+01;	
Matches	11; Conservative	10;	Mismatches	18;	Indels
Gaps	0;				

RESULT	15	standard; Protein; 576 AA.
ID	R66929	
AC	R66929;	
DT	01-SEP-1995	(first entry)
DE	AMML chromosome inv(16) product.	
KM	AMML; acute myelomonocytic leukemia; chromosome-16; inversion;	
KM	inv(16); CBF-beta; CBFb gene; transcription factor; myosin; MYH11;	
KM	SMHHC.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	Peptide	1..164
FT	/label= CBFb	
FT	Peptide	165..576
FT	/label= MYH11	
PN	M09504067-A.	
PD	09-FEB-1995.	
PF	26-JUL-1994; U08530.	
PR	29-JUL-1993; U5-099869.	
PA	(UNMI) UNIV MICHIGAN.	
PA	(TEXA) UNIV TEXAS SYSTEM.	
PI	Claxton D, Collins FS, Liu P, Siciliano MJ;	
DR	WPI; 95-082178/11.	
DR	N-PSDB; Q84588.	
PT	Novel DNA spanning the pericentric inversion of chromosome 16 -	
PT	for the screening of acute myeloid Leukemia	
CC	Claim 4; Page 28-30; 78pp; English.	
CC	PCR was performed on total cellular RNA from 5 AMML patients having	
CC	a pericentric inversion of chromosome-16, MdeO subtype. Sequencing	

Dec 10 06:53

US-08-446-915-4.r8g

下

CC showed the *inv(16)* fusion to comprise a sequence from the *CBFβ*
CC gene, encoding a novel transcription factor, and the *MYH11* gene,
CC encoding smooth muscle myosin heavy chain. In 3 patients, nt 1-492
CC of the *CBFβ* gene were fused to nt 1921 of *MYH11* (shown in
CC Q84588), predicted as sequence in R66929). Probes based on *inv(16)*
CC can be used for diagnosis of AMLt..
CC Sequence 576 AA;
CC

Db 414 erstcaqknesarqr-larqnke-lrsklhmeagavaksfxttaaleakiqdle 465
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Qy 294 EKVAVTLEAKSRQHRLLPDDLTALSNKKVQDLNLSIGLK-DLAADVDLKRVSLE 346
 Matches 16; Conservative 20; Mismatches 15; Indels 3; Gaps 3.

Search completed: Tue Dec 10 07:09:39 1996
Job time : 58 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 10 07:04:40 1996; MsePar time 9.40 Seconds

414.306 Million cell updates/sec

Tabular output not generated.

Title: >US-08-446-915-2

Description: (1-409) from US08446915.pep

Perfect Score: 2945

Sequence: 1 MASSSADPENEQFCGPAP.....KRAYKDDTMEIKCIQDTSA 409

Scoring table: PAM 150

Gap 11

Searched: 81589 seqs, 9523651 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq24

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 34.957; Variance 160.267; scale 0.218

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	length	DB	ID	Description	Pred. No
1	2945	100.0	409	15	R90577	Mouse TRAF1.	1.47e-259		
2	972	33.0	501	15	R90578	Mouse TRAF2.	7.66e-76		
3	112	3.8	870	6	R31348	Jaagsiekte retrovirus	1.77e+00		
4	113	3.8	1427	2	R10534	Human 160KD mediator	1.51e+00		
5	105	3.6	383	12	R62636	Petunia Pth gene prod	5.43e+00		
6	103	3.5	192	12	R62757	SetU2 sequence.	7.45e+00		
7	103	3.5	509	5	R30429	Major Yo paraneoplas	7.45e+00		
8	99	3.4	77	6	R32698	SSP polypeptide produ	1.39e+01		
9	99	3.4	77	16	R18258	SSP 7.7,7.7.7.8.9.8	1.39e+01		
10	101	3.4	430	5	R26173	Part of Major Yo para	1.02e+01		
11	101	3.4	738	15	R69851	Ethylene response (ET	1.02e+01		
12	101	3.4	738	15	R69852	Ethylene response (ET	1.02e+01		

13	101	3.4	738	15	R69853	Ethylene response (ET	1,02e+01
14	101	3.4	738	15	R69849	Ethylene response (ET	1,02e+01
15	101	3.4	738	15	R69850	Ethylene response (ET	1,02e+01
16	100	3.4	1093	8	R42818	TNF.	1,19e+01
17	94	3.2	405	11	R57499	Human variant cortico	3,00e+01
18	93	3.2	405	11	R57498	Human corticosteroid	3,49e+01
19	93	3.2	405	11	R61174	Corticosteroid bindin	3,49e+01
20	93	3.2	444	16	R86801	T. thermophilus gamma	3,49e+01
21	95	3.2	1618	5	R27205	Human nestin.	2,57e+01
22	95	3.2	1618	11	R60127	Human nestin protein	2,57e+01
23	92	3.1	235	1	P94260	41kD protein of T. co	4,06e+01
24	92	3.1	320	1	P94366	41kD protein of T. co	4,06e+01
25	92	3.1	362	8	R41536	Preprokinin 2 toxin	4,06e+01
26	90	3.1	394	16	R94559	Human Gs alpha protei	5,47e+01
27	92	3.1	462	1	R05766	Portion of peptide an	4,06e+01
28	91	3.1	476	8	R43563	Hyaluronan receptor.	4,77e+01
29	90	3.1	648	16	R94906	RAP-1 radiation prote	5,47e+01
30	92	3.1	955	11	R57365	K39 polypeptide of Le	4,06e+01
31	90	3.1	1147	8	R41199	CAI antigen.	5,47e+01
32	91	3.1	15281	8	R49429	T. nkrvum Cyclosporin	4,77e+01
33	88	3.0	239	2	R04117	ORF2 of Enod2a genom	7,37e+01
34	88	3.0	239	2	R04118	ORF1 of Enod2b genom	7,37e+01
35	88	3.0	433	2	R08335	CD4.	7,37e+01
36	88	3.0	435	2	P90992	Human CD4 antigen	7,37e+01
37	88	3.0	435	2	P91289	Sequence of a segment	7,37e+01
38	89	3.0	615	15	R74630	Tomato TGEV1 ethylen	6,35e+01
39	88	3.0	816	12	R66931	AMM chromosome inv(1	7,37e+01
40	88	3.0	885	12	R66930	AMM chromosome inv(1	7,37e+01
41	88	3.0	897	16	R92751	Marine EGF receptor s	7,37e+01
42	88	3.0	1365	6	R36780	KRES.	7,37e+01
43	88	3.0	1764	1	P91672	Primary amino acid se	7,37e+01
44	89	3.0	2101	8	R47173	Sequence of the inner	6,35e+01
45	88	3.0	5035	5	R25450	MH mutant porcine rya	7,37e+01

ALIGNMENTS

RESULT	1	
ID	R90577	standard; Protein; 409 AA.
AC	R90577;	
DT	09-APR-1996	(first entry)
DE	Mouse TRAF1.	
KW	TRAF1; tumour necrosis factor receptor associated factor 1;	
KW	TNF; CD40.	
OS	Mus musculus.	
FH	Key	Location/Qualifiers
FT	Domain	180..409
FT	/label= TRAF_domain	
FT	Region	183..259
FT	/label= leucine_zipper_region	
PN	W09533051-A1.	
PD	07-DEC-1995.	
PF	25-MAY-1995;	U06639.
PR	27-MAY-1994;	US-250858.
PR	28-OCT-1994;	US-331394.
PR	22-MAY-1995;	US-446915.
PA	(GETH) GENENTECH INC.	
PI	Goeddel DV; Roche M	
DR	WPI; 96-049310/05.	
DR	N-PSDB; T1261.	
PT	Tumour necrosis factor (TNF) receptor-associated factors - involved	
PT	in mediation of biological activities of TNF and CD40 ligands	
PS	Claim 8; Page 71-72; 116pp; English.	
CC	Mouse tumour necrosis factor receptor associated factor 1 (TRAF1)	

CC See also R31346-7, R31349 and Q35153-Q35155.
SQ Sequence 870 AA;

Query Match 3.8%; Score 112; DB 6; Length 870;
Best Local Similarity 24.7%; Pred. No. 1.77e+00;

Matches 24; Conservative 27; Mismatches 42; Indels 4; Gaps 4;

Db 187 qlylvhnddllahtcdhl-lygaf-ealkqlstngvladekltqthfpyylygfsl 244
:| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |

Qy 168 ELALQHLVKEKLLAQLEEKLFNFNIYAVLKEVEASHLALASTHQSQLDREHL-LSTLE 226

Db 245 pryntqlvklqfcdh-lktlndfgkljgdmwtrpyl 280
|| : | | : | | : | | : | | : | | : | | : | | : | | : | |

Qy 227 QRVEIQAQTIAQKQDVAKGKLESHRLMEKASFTDTFL 263

RESULT 4

ID R10534 standard; Protein; 1427 AA.

AC R10534;

DT 12-APR-1991 (first entry)

DE Human 160kD mediator of inflammation protein.

KM Mediator of inflammation; cytokine; Hodgkin's lymphoma; MRP-160.

OS Homo sapiens.

PN EP-412050-A.

PD 06-FEB-1991.

PF 26-JUN-1990; 810481.

PR 05-JUL-1989; GB-015414.

PA (CIBA) CIBA GEIGY AG.

PI odink KG, Tarcsey L, Bruggen J, Wiesendanger W, Cerletti N;

PI Sorg C, Dewolf-Peters C, Delabie J;

DR WPI; 91-038913/06.

DR N-PSDB; Q10378.

PT 160 kD human polypeptide mediator or precursor of inflammation -

PT polyclonal or monoclonal antibodies to polypeptide treat and

PT diagnose chronic inflammation and hodgkins lymphoma

PS Claim 3; Page 32; 47pp; English.

CC The protein is a cytokine used to treat chronic inflammatory

CC conditions. It is prepared by chromatographically purifying an

CC optionally pre-purified cell extract, cell supernatant or cell

CC filtrate of stimulated normal human leucocytes or human embryonic

CC epithelial lung cells. Alternatively, the protein can be produced

CC by microorganisms or continuous mammalian cell lines, transformed

CC with plasmids encoding MRP-160. The invention also covers the

CC polypeptide fragment from amino acids 878-1427 and derivatives of

CC the protein in which the amino and/or hydroxyl functions are

CC glycosylated or acylated and have mol. wt.s of 190 and 140kD,

CC respectively.

SQ Sequence 1427 AA;

Query Match 3.8%; Score 113; DB 2; Length 1427;
Best Local Similarity 25.0%; Pred. No. 1.51e+00;

Matches 24; Conservative 31; Mismatches 34; Indels 7; Gaps 7;

Db 451 tkgdletqtklehari-kelegsl-lfektacklqreledtravtvekselmelekl 508
:| | : | | : | | : | | : | | : | | : | | : | | : | |

Qy 165 SQEELALQ-HLVKEKLLAQLEEKLFNFNIYAVLKEVEASHLALASTHQSQLDREH 221

Db 509 alrvqe-vaelrrrl-esnkpadvdmslellgeis 542
| : | : | : | : | : | : | : | : | : | : | : | : |

Qy 222 LLSLEQRVEIQAQTIAQKQDVAKGKLESHRLMEKAS 257

RESULT 5

ID R62656 standard; Protein; 383 AA.

AC R62656;
DT 08-JUN-1995 (first entry)

DE Petunia Ph6 gene product.

KM Vacuolar pH; pH gene; Petunia.

OS Petunia hybrida strain V26.

FH Key Location/Qualifiers

FT Region 192..198

FT /label= Helix-loop-helix structural motif

FT /note= "see also 239..245"

PN W09423561-A.

PD 27-OCT-1994.

PF 15-APR-1994; U04173.

PR 16-APR-1993; US-049282.

PA (DNAP) DNA PLANT TECHNOLOGY CORP.

PI Chuck GS, Courtney-guterson N, Dooner HK, Keller J;

PI Nijjar CS, Ralston EJ;

DR WPI; 94-341349/42.

DR N-PSDB; Q73000.

PT Petunia Ph gene and constructs containing it - for alteration of

PT vacuolar pH used in the formation of blue flowers

PS Disclosure; Page 42-44; 62pp; English.

CC The V26 strain of Petunia was used. Poly A RNA was isolated from

CC total RNA from flower buds and used to generate a cDNA library in

CC the vector lambda ZapII (Stratagene). The SstI to BamHI fragment at

CC the left hand side of Ac was used to isolate pPet14-1 (contg. pH6

CC cDNA), the sequence for which is claimed (see Q73000 FT). The AA

CC sequence comprises a helix-loop-helix structural motif starting with

CC the sequence NHVLAER (starting at residue 192) and extending to the

CC motif include the myc family of oncogenes, regulators of neuron and

CC muscle development, and regulators of segmentation and organ

CC patterning in Drosophila. In plants, the motif is found in R(S),

CC a protein involved with regulating anthocyanin synthesis in Maize.

CC Comparison of the pH6 and R(S) sequences over the 54 AA helix-loop-

CC helix region detected 57% AA identity. Outside this region only 19%

CC identity was found.

SQ Sequence 383 AA;

Query Match 3.6%; Score 105; DB 12; Length 383;
Best Local Similarity 27.1%; Pred. No. 5.43e+00;

Matches 23; Conservative 25; Mismatches 32; Indels 5; Gaps 5;

Db 178 frkgsctqpepsqnhvlaerrrcklnerfllrslypvtck-mdkasi-ldtleyvk 235
:| | : | | : | | : | | : | | : | | : | | : | | : | |

Qy 158 YRAPCCSQEELALQHLVKEKLLAQ-LEEKLFNFNIYAVLKEVEASHLALASTH-QS 215

Db 236 ql-rtkhvgdlearangteartlqtld 259
|| | : || | : : || |

Qy 216 QLDREHLSTLEQRVEIQAQTIAQKD 240

RESULT 6

ID R62757 standard; Protein; 192 AA.

AC R62757;

DT 26-JUN-1995 (first entry)

DE SetU2 sequence.

KM Salmonella; SetU2; vaccine.

OS Salmonella.

PN W09425598-A.

PD 10-NOV-1994.

PF 26-APR-1994; I80207.

PR 26-APR-1993; US-054452.

PA (KING/) KING J.

PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

KM	Ethylene response; recombinant; mutation; decrease; fruit ripening;
KW	abscission; floral senescence.
OS	Arabidopsis thaliana.
PN	W09501439-A2.
PD	12-JUN-1995.
PE	30-JUN-1994; 007418.
PR	01-JUL-1993; US-086555.
PR	28-JUN-1994; US-263480.
PA	(CALY) CALIFORNIA INST OF TECHN.
PI	Bleecker AB, Chang C, Meyerowitz EM;
DR	WPI; 95-061003/08.
DR	N-PSDB; Q85539.
PT	Modified ethylene response (ETR) nucleic acid - useful for producing
PT	transformed plants with decrease in response to ethylene
PS	Claim 2; Page 71-74; 21pp; English.
CC	R69850-669853 represent the amino acid sequences of the Arabidopsis
CC	thaliana mutated ethylene response (ETR) proteins etrl-1, etrl-2,
CC	etrl-3 and etrl-4 respectively. The cDNA sequences which encode
CC	these proteins can be linked to a promoter and used to transform
CC	plant cells of fruit bearing plants (in partic. the fruit is a
CC	tomato) resulting in a decrease in response to ethylene. This enables
CC	controlled fruit ripening and delayed floral senescence and
CC	abscission during growth, transport or storage.
CC	Sequence 738 AA;

	Query Match	3.4%	Score 101;	DB 15;	Length 738;
	Best Local Similarity	26.8%	Pseq. No. 1.02e+01;		
	Matches 30; Conservative		Mismatch. 36;	Indels 9;	Gaps 7;
D b	321 dllmegmalalareeeacfarandflammbentprmaiaaislsgtelcpqrql				380
	: : :: : : : : : : : : : : : : : : : : : :				
Oy	168 ELALQHLVKEKILAQLEEK-LVFANFANIYAAVKVEAS-N--IALMASIHQSIDREHLL				223
D b	381 mveitlkseallatlamdvldstriedgsl-qelqglntlnhtlfrevnlmk				431
	: : : : : : : : : : : : : : : : : : :				
Oy	224 SLSD--RVELDQQTIAKKOQIVAGKIEH-SIRLMEEASPD-GTEIMKTINVRK				271

RESULT	12
ID	R69852 standard; Protein; 738 AA.
AC	R69852;
DT	21-MAR-1996 (first entry)
DE	Ethylene response (ETR) mutant protein etrl-3.
KW	Ethylene response; recombinant; mutation; decrease; fruit ripening;
KW	abscission; floral senescence.
OS	Arabidopsis thaliana.
PN	W09501439-A2.
PD	12-JAN-1995.
PF	30-JUN-1994; U07418.
PR	01-JUL-1993; U5-086555.
PR	28-JUN-1994; U5-263480.
PA	(CALY) CALIFORNIA INST OF TECHN.
PI	Bleeker AB, Chang C, Meyerowitz EM,
DR	WPI; 95-061003/08.
DR	N-PSDB; 085560.
PT	Modified ethylene response (ETR) nucleic acid - useful for producing
PT	transformed plants with decrease in response to ethylene
PS	Claim 2; Page 76-80; 21Dp; English.
CC	R69850-R69853 represent the amino acid sequences of the Arabidopsis
CC	thaliana etrl-4 mutant ethylene response (ETR) proteins etrl-1, etrl-2,
CC	etrl-3 and etrl-4 respectively. The cDNA sequences which encode
CC	these proteins can be linked to a promoter and used to transform
CC	plant cells of fruit bearing plants (in partic. the fruit is a
CC	tomato) resulting in a decrease in response to ethylene. This enables

CC controlled fruit ripening and delayed floral senescence and
CC abscission during growth, transport or storage.
SQ Sequence 738 AA;

Query Match 3.4%; Score 101; DB 15; Length 738;
Best Local Similarity 26.8%;
Matches 30; Conservative 36; Mismatches 37; Indels 9; Gaps 7;

D**b** 321 dllneqvaldarceaeairandflwamchertpmhaialaslgeltetpeqr 380
 :|:::| | | :| :| ::::|||:| :| :| :|:::|:::| :| :|
Q**y** 168 ELAIDHLYEKELIALEEK-LNFVANIYAVLNKEVAS-N--IALAAISHQSIDREBHL 223
 :|:::| | | :| :| ::::|||:| :| :| :|:::|:::| :| :|

D**b** 381 mveltksnllaImndvlsrldsgdsq-elgufnhtlfrevnlll 431
 :| :| :| | | | | | | | | | | :| :| :| :| :| :| :| :|
Q**y** 224 SLEDG-RVEELDQTLAKDQVAGLKEH-SRLMEASDS-GTDLKNTNVR 271
 :| :| :| | | | | | | | | | | :| :| :| :| :| :| :| :|

RESULT	13	
ID	R69853	standard; Protein; 738 AA.
AC	R69853;	
DT	21-MAR-1996	(first entry)
DE	Ethylene response (ETR) mutant protein etrl-4.	
KW	Ethylene response; recombinant; mutation; decrease; fruit ripening;	
KW	abscission; floral senescence.	
OS	Arabidopsis thaliana.	
PN	W09501439-A2.	
PD	12-JAN-1995.	
PF	30-JUN-1994; 007418.	
PR	01-JUL-1993; US-086555.	
PR	28-JUN-1994; US-263480.	
PA	(CALY) CALIFORNIA INST OF TECHN.	
PI	Bleecker AB, Chang C, Meyerowitz EM;	
DR	WPI; 95-061003/08.	
DR	N-P5DB; 085561.	
PT	Modified ethylene response (ETR) nucleic acid - useful for producing	
PT	transformed plants with decrease in response to ethylene	
CS	Claim 2; Page 82-86; 212pp; English.	
CC	R69850-R69883 represent the amino acid sequences of the Arabidopsis	
CC	thaliana mutated ethylene response (ETR) proteins etrl-1, etrl-2,	
CC	etrl-3 and etrl-4 respectively. The cDNA sequences which encode	
CC	these proteins can be linked to a promoter and used to transform	
CC	plant cells of fruit bearing plants (in partic. the fruit is a	
CC	tomato) resulting in a decrease in response to ethylene. This enables	
CC	controlled fruit ripening and delayed floral senescence and	
CC	abscission during growth, transport or storage.	
SQ	Sequence 738 AA;	
Query Match	3.4%; Score 101; DB 15; Length 738;	
Best Local Similarity	26.8%; Pred. No. 1.02e+01;	
Matches	30; Conservative 36; Mismatches 37; Indels 9; Gaps 7;	
Db	321 dlmegvaldlarreseafarndflamhnmhmtahialesllgetlpegrl 380	
QY	: ::	
	168 ELALQHVKEKILQAEEK-LVFRNIVAVINKEVNS-H-LATAASTHQSQDRHLL 223	
Db	381 mvelilksnllatlmndvldstrldsglq-elgtfnhtlffrevlnlkl 431	
QY	:	
	224 SLEQ-RVEIQQTIAKQDVIGKLEH-SRLMEFASPD-GTFIMKTNVTK 271	
RESULT	14	
ID	R69849	standard; Protein; 738 AA.
AC	R69849;	
DT	20-MAR-1996	(first entry)

DE Ethylene response (ETR) gene product.
KM Ethylene response; recombinant; mutation; decrease; fruit ripening;
KM abscission; floral senescence.
OS Arabidopsis thaliana.
PN W09501439-A2.
PD 12-JAN-1995.
PF 30-JUN-1994; U07418.
PR 01-JUL-1993; US-086555.
PR 28-JUN-1994; US-263480.
PA (CALY) CALIFORNIA INST OF TECHN.
P1 Bleeker AB, Chang C, Meyerowitz EM;
DR WPI; 95-061003/08.
DR N-PSDB; Q85557.
PT Modified ethylene response (ETR) nucleic acid - useful for producing
PT transformed plants with decrease in response to ethylene
PS Claim 1; Page 59-62; 212pp; English.
CC Q85557 represents the cDNA sequence of the Arabidopsis thaliana
CC ethylene response (ETR) gene which codes for the ethylene response
CC protein (R69849). The ETR cDNA or the full gene sequence (Q85556)
CC can be mutated and linked to a promoter and used to transform plant
CC cells of fruit bearing plants (in partic. the fruit is a tomato)
CC resulting in a decrease in response to ethylene. This enables
CC controlled fruit ripening and delayed floral senescence and
CC abscission during growth, transport or storage.
SQ Sequence 738 AA;

Query Match 3.4%; Score 101; DB 15; Length 738;
Best Local Similarity 26.8%; Pred. No. 1.02e+01;
Matches 30; Conservative 36; Mismatches 37; Indels 9; Gaps 7;

Db 321 dlimegnvaldlarreatairardflavmhemtprmhailalsllgeteltpgrl 380
:|::| | | : | :| ::||:| | :| :|:::|::| | :|
Qy 168 ELALQHLVKEKLLAQLEEK-LRFFANIVAVLNKEVAS-H--LALAASIHQSQDREHLL 223
:
Db 381 mvetllksnllatlmndvldarledgsqql-elgtfnlhtlfrevnlilk 431
:
Qy 224 SLEQ--RVEELQDTLAQKQVLEKLEH-SLRIMEASFD-CTFLMKITVTK 271

RESULT 15
ID R69850 standard; Protein; 738 AA.
AC R69850;
DT 20-MAR-1996 (first entry)
DE Ethylene response (ETR) mutant protein etrl-1.
KM Ethylene response; recombinant; mutation; decrease; fruit ripening;
KM abscission; floral senescence.
OS Arabidopsis thaliana.
PN W09501439-A2.
PD 12-JAN-1995.
PF 30-JUN-1994; U07418.
PR 01-JUL-1993; US-086555.
PR 28-JUN-1994; US-263480.
PA (CALY) CALIFORNIA INST OF TECHN.
P1 Bleeker AB, Chang C, Meyerowitz EM;
DR WPI; 95-061003/08.
DR N-PSDB; Q85558.
PT Modified ethylene response (ETR) nucleic acid - useful for producing
PT transformed plants with decrease in response to ethylene
PS Claim 2; Page 65-68; 212pp; English.
CC R69850-R69853 represent the amino acid sequences of the Arabidopsis
CC thaliana mutated ethylene response (ETR) proteins etrl-1, etrl-2,
CC etrl-3 and etrl-4 respectively. The cDNA sequences which encode
CC these proteins can be linked to a promoter and used to transform
CC plant cells of fruit bearing plants (in partic. the fruit is a

CC tomato) resulting in a decrease in response to ethylene. This enables
CC controlled fruit ripening and delayed floral senescence and
CC abscission during growth, transport or storage.
SQ Sequence 738 AA;

Query Match 3.4%; Score 101; DB 15; Length 738;
Best Local Similarity 26.8%; Pred. No. 1.02e+01;
Matches 30; Conservative 36; Mismatches 37; Indels 9; Gaps 7;

Db 321 dlimegnvaldlarreatairardflavmhemtprmhailalsllgeteltpgrl 380
:|::| | | : | :| ::||:| | :| :|:::|::| | :|
Qy 168 ELALQHLVKEKLLAQLEEK-LRFFANIVAVLNKEVAS-H--LALAASIHQSQDREHLL 223
:
Db 381 mvetllksnllatlmndvldarledgsqql-elgtfnlhtlfrevnlilk 431
:
Qy 224 SLEQ--RVEELQDTLAQKQVLEKLEH-SLRIMEASFD-CTFLMKITVTK 271

Search completed: Tue Dec 10 07:06:11 1996
Job time : 91 secs.